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P12844 caenorhabdi
Q02455 saccharomyc
Q59996 ha-kinase
P29616 gallus gall
P12749 homo sapien
P27793 ovis aries
Q9u6a1 drosophila
P02563 rattus norv
Q13439 homo sapien
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RT cultured cells.";

RT cultured cells.";

RT cultured cells.";

RT cultured cells.";

RT J. Biol. Chem. 277:27757-27764 (2002).

CC i- FUNCTION: probably plays a role in the formation and regulation of CC cells to the tight junction (TJ) paracellular permeability barrier, the tight junction (TJ) paracellular permeability barrier, composibly by linking ZO proteins to the actomyosin cytoskeleton. CC cells and ZO-3, myosin and cocludin in vitro, possibly cells on vivo, and ZO-3, myosin and cocludin in vitro, possibly cells cells.

CC directly. Acts as an F-actin bundling protein in vitro. CC directly. BecIFICITY: Localized on the cytoplasmic face of tight cells. CC cells beptihelia and some endothelia. Found in CC cells cells in the fertilized egg, where it is associated cells apical cortex in the fertilized egg, where it is associated with cytoskeleton filaments, it is recruited to tight junctions before ZO-1 and occludin. Nascent tight junctions are in place by the two-cell stage.

CC -- DOWAIN: Deletion of the ZO-1 interaction motif (ZIM) decreases but CC -- DOWAIN: Deletion of the ZO-1 interaction with ZO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordenonsi M., D'Atri F., Hammar E., Parry I
Shore D., Citi S.;
"Cingulin contains globular and coiled-coil
ZO-1, ZO-2, ZO-3 and myosin.";
J. Cell Biol. 147:1569-1581(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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MEDLINE=20082893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cordenonsi M., Turco F., D'Atri F., Hammar E., Martinucci G., Cordenonsi M., Turco F., D'Atri F., Hammar E., Martinucci G., Meggio F., Citi S.;
Meggio F., Citi S.;
"Xenopus laevis occludin. Identification of in vitro phosphorylation "Xenopus laevis occludin. Identification of in vitro phosphorylation sites by protein kinase CK2 and association with cingulin.";
sites by protein kinase CK2 and association with cingulin.";
Bur. J. Biochem. 264:374-384(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION IN TIGHT JUNCTION BIOGENESIS. MEDLINE=20400099; PubMed=10940624; Pesenko I., Kurth T., Sheth B., Fleming "Tight junction biogenesis in the early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardellini P., Davanzo G., Citi S.;
"Tight junctions in early amphibian development: detection of
"unctional cingulin from the 2-cell stage and its localization at the
boundary of distinct membrane domains in dividing blastomeres in low
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=21538627; PubMed=11682052;
D'Atri F., Citi S.;
"Cingulin interacts with F-actin i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99421641; PubMed=10491082;
Cordenonsi M., Turco F., D'Atri F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       D'Atri F., Nadalutti F., Citi S.; "Evidence for a functional interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS
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between the Swiss Institute of Bioinformatics and the EWBL
the European Bioinformatics Institute. There are no restrict
use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lett. 507:21-24(2001).
                                                                                                     DOMAIN: Deletion of the ZO-1 interaction motif (ZIM) does not abolish colocalization with ZO-1.
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Xenopus embryo.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRELAEV------LEKDLQMRGASVIPCGEIYGQWKGLG
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HEEIFDLEKE
                                                               VVGQQQQNINPSSNDDCRKRAEEVSSF1EFQEKEMEEFVEEREMLIKDQEKKMEDMKKRH
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                               LKGTLKEEVSGRDRETVRLR-EQLQSEVMHVKKENEGLAKESRR-IQDQLKQVLLEKQRH
                                                                                                 SLLQSELAQVKKGSVDPGEVASVRKELQRVQDQLKQLSVDKQKVEEN--
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RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschal S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Robrigger J., Worley R.C., Shevchenko Y., Bouffard G.G.,

RA Rodrigger A.C., Schein J.W., Green E.J., Lu X., Gibbs R.A.,

RA Rodrigger A.C., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

"Generation and mouse cDNA sequences"."

"Generation and mouse cDNA sequences"."

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"Generation and regulation of the tight junction (TJ) paracellular permeability barrier (By

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"Generation and regulation of the tight junction (TJ) paracellular permeability barrier (By
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                    GG; GO:0005923; C:tight junction; NAS
GG; GO:0003779; F:actin binding; ISS.
InterPro: IPR002928; Myosin tail.
Pfam; PF01576; Myosin tail; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homodimer. Interacts with TJP1/ZO-1 (By similarity). DOMAIN: Deletion of the ZO-1 interaction motif (ZIM) decreases does not abolish colocalization with ZO-1 (By similarity).
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Similarity 18.9%;
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; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
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                                  Score 183; DB 1; Length 1191; Pred. No. 0.025;
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DT 15-MAR
DE Bromod

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BY HUMAN STANDARD; PRT; 1972 AA Q9UIF8; Q96EA1; Q96SQ8; Q9P252; Q9Y4N8; Q8-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation updat. Bromodomain adjacent to zinc finger domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V$QN$NPPRAWGGQQQGRGSNVSGRGNNVSGRGNGNGRGI----QANISG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSGRRPARDARASTYGVAVRVQGIAGQPFVVLNSGEKGTDSFGVQIKGGNNRGSPGA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGSLDS-----LSIEQINEP-------QRQWHCPACQNGPGAIDWY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMGNQELLEYFDKYEALRARHSYG-PQGHRGMSVLMFESSATGYLEAER------LH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -lapkptssintidtaplssydslinkfdsokgg---ovrgrtgrrt--r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -QSMFQKNKEEL---RATKQEL---LQLRMEKEEMEEELGEKMEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NLHPL--LAHARTKG-ARRVKLHRELAEV------
                                                                                                                                                                                                                                                                                                                                                                                                                    -GQQQQNINPSSNDDCRKRAEEVSSFIEFQE-----
          ion update)
c domain 2B
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                 (hWALp4).
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                            KX MEDULINE=2238023; FUNDWEUT=144 //3740.

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Generation and initial analysis of more than 15,000 full-length

RA Mitchell Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Mitchell Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Mitchell Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Mitchell Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Mitchell Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Mitchell Y.S.N., Krzywinski M.I., Skals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20277482; PubMed=10819331;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"prediction of the coding sequences of unidentified human ger
The complete sequences of 100 new cDNA clones from brain whic
for large proteins in vitro.";
DNA Res. 7:143-150(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAZ2B OR KIAA1476
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Ohara O., Nagase T.,
Submitted (APR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones M.H., Hamana N., Nezu J., Shimane "A novel family of bromodomain genes."; Genomics 63:40-45(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 753-1972 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-776 FROM N.A. (ISOFORM
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                                                                                                                                                                                                                                                                                      Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Yasaho Y., Kanehori K.;
                                                                                                                                                      Submitted (JUN-1999)
                                                                                                                                                                                               TISSUE=Testis;
                                                                                                                                                                                                              SEQUENCE OF 1524-1972
                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                             "NEDO human
                                               stka A., Klein M., Mewes H.-W., Gassenhuber J., Wien mitted (JUN-1999) to the EMBL/GenBank/DDBJ databases FUNCTION: May play a role in transcriptional regula interacting with ISWI.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JUL-2002) to
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a N., Nezu J., Shimane M.;
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the EMBL/GenBank/DDBJ
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    R.;
    EMBL/GenBank/DDBJ

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EMBL/GenBank/DDBJ
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databases.
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databases
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PRINTS; PRO0563; BROMODOMAIN.
SMART; SM00297; BROMO; 1.
SMART; SM00297; BROMO; 1.
SMART; SM00291; MBD; 1.
SMART; SM00391; MBD; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
PROSITE; PS50014; BROMODOMAIN_2; 1.
PROSITE; PS50014; BROMODOMAIN_2; 1.
PROSITE; PS50015; ZF_PHD_1; FALSE_NEG.
PROSITE; PS01359; ZF_PHD_1; FALSE_NEG.
PROSITE; PS01359; ZF_PHD_2; 1.
Transcription_regulation_Bromodomain; Zinc-f.
                                          DOMAIN
ZN FING
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EMBL; AB040909; BAA96000.2; ALT_INIT.
EMBL; AL834381; CAD39044.1; ALT_INIT.
EMBL; BC012576; AAH12576.1; ALT_FRAME.
***??77412: BAB55231.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK027612; BAB55231.1;
EMBL; AL080173; CAB45759.1;
PIR; T12495; T12495.
             VARSPLIC
                                                                                                                                                                                                                                                                                                                               Pfam; PF00439;
                                                                                                                                                                       Nuclear
                                                                                                                                                                                                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Q92831;
                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001487; Bromodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 bromodomain.

SIMILARITY: Contains 1 DDT domain.

SIMILARITY: Contains 1 methyl-binding (MBD) domain.

SIMILARITY: Contains 1 PHD-type zinc finger.

CAUTION: Ref.5 sequence differs from that shown due frameshift in position 731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the WAL family. SIMILARITY: Contains 1 bromodomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9UIF8-3; Sequence=VSP_000554;
Note=Inferred from Ref.5;
TISSUE SPECIFICITY: Expressed at varying levels in several tissues, whereas a smaller transcript was expressed specif
                                                                                                                                                                                                                                                                                                                                                                                     605683;
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                                                                                                                                                                                                                                                                                                                                                                                            HGNC:963; BAZ2B.
                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                         IPR004022; DDT_dom.
IPR001739; Methyl-CpG_bind.
IPR001965; Znf_PHD.
                                                                                                                           891
1735
1881
                                                                                                                                                                                                                                                                                               ; bromodomain; 1.
; DDT; 1.
; MBD; 1.
; PHD; 1.
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                                                                                                                                                                    DNA-binding;
                                          470
672
865
875
1143
1179
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rom Ref.4;
                                                                                                                                                                               Bromodomain; Zinc-finger; Coiled
 ASP-RICH.
COILED COIL (POTENTIAL).
Missing (in isoform 2).
/FTId=VSP 000553.
Missing (In isoform 3).
/FTId=VSP_000554.
                                                                 LYS-RICH.
                                                                        ARG-RICH.
COILED COIL (POTENTIAL).
                                                                                                                   SER-RICH.
                                                                                                                            PHD-TYPE.
BROMODOMAIN.
                                                                                              ASP/GLU-RICH
                                                                                                        POLY-GLU
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                               isotorm 2).
                                            (POTENTIAL)
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SEQUENCE FROM N.A.
TISSUE=Neuroepithelium;
                              NCBI_TaxID=9606;
                                                                                             10-OCT-2003
                                                                                                                                      CING_HUMAN
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Q9P2M7; Q9NR25;
28-FEB-2003 (Rel
28-FEB-2003 (Rel
                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                       Cingulin.
CGN OR KIAA1319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514 SESQSPAFLGTSSSTLTSSPHSGTSKRRRVTDERELRIPLEYGWQRETRIRNFGGRLQGE
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s (Human).

Metazoa; Chordata; C

Metazoa; Primates; (
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
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Pred. No. 0.063;
                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                    PRT;
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Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O
"Prediction of the coding sequences of unidentified human
The complete sequences of 150 new cDNA clones from brain w
for large proteins in vitro.";
NA Res. 7:65-73(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20499514; PubMed=11042084; Citi S., D'Atri F., Parry D.A.D.; "Human and Xenopus cingulin share a coiled-coil rod domain: predictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assembly.";
J. Struct. Biol. 131:135-145(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22140336; PubMed=12023291;
D'Atri F., Nadalutti F., Citi S.;
"Evidence for a functional interaction between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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J. Biol. Chem. 2
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                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002928; Myosin_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUNCTION: Probably plays a role in the formation and regulation the tight junction (TU) paracellular permeability barrier: the tight junction (TU) paracellular permeability barrier: SUBUNIT: Homodimer (By similarity). Interacts with TUFI/ZO-1. SUBUNIT: Homodimer (By similarity). Interacts with TUFI/ZO-1. TISSUE SPECIFICITY: Localized on the cytoplasmic face of tight punctions of polarized epithelia and some endothelia. Expressed junctions of polarized epithelia and some endothelia. Expressed junctions, kidney, liver and lung, but not in skeletal muscle, pancreas, kidney, liver and lung, but not in skeletal muscle, placenta, brain or heart.

DOMAIN: Deletion of the ZO-1 interaction motif (ZIM) decreases b does not abolish colocalization with ZO-1.
                                                                                                                                                                                                                                                                                                                                                     GO:0005923; C:tight junction; NAS: GO:0003779; F:actin binding; ISS: GO:0005515; F:protein binding; IPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ev
                                                                                                                                                                                                                                                                                                                                                                                          AF263462; AAF74498.1; ALT_INIT.
AB037740; BAA92557.1; ALT_INIT.
; HGNC:17429; CGN.
                                                                                                                                                                                                                                                                                                                            PF01576; Myosin
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                                                                                                                                                                           Similarity
                                                                                                       RGGRRPAKDARASTYGVAVRVÓĞIÁĞQPFVVLNSGEKGGDSFGVQIKGANDQG-ASGA--
                                                                               V$QNSNPPRAWGGQQQGRGSNVSGRGNNVSGRGNGNGRGI----QANISGRGRALSRKYD
  NNFV-APPPVSRP-----PLE-----
                                                   Conservative
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ZIM.
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COILED
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Pred. No. 0.046;
                                                                                                                                                                                                                      INTERACTS WITH ZO-2.
W; 0C9375283ABAAF3D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modular organization of the for intra- and intermolecular
                                                                                                                                                                                                                                                                                          COIL
                               -----GGWNWQARGGSAQHTAVQEFPDVE 158
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from brain which co
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MBL outstation -
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SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
TISSUE-Skeletal muscle;
MEDLINE-90323631; PubMed=2373371;
MEDLINE-90323631; PubMed=2373371;
Karsch-Mizrachi I., Peghali R., Showe
"Generation of a full-length human peencoding cDNA.";
                                                                                                                                                                                                                                                                                                                            MYH8 HUMAN
P13535; Q149
01-JAN-1990
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15-771-1598 (Rel. 36, Last sequence up
15-771-1998 (Rel. 43, Last annotation
15-771-1998 (Rel. 43, Last annotation
Myosin heavy chain, skeletal muscle, p
                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                Myosin heavy
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                                                                                                                                                                                                                              (Human)
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Primates;
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                          perinatal
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perinatal
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                                                                T.B.
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                                                                Jr.,
                                            myosin heavy
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                                                                                                                                                                                                                     Euteleostomi
                                                 nwand L.A.;
heavy-chain-
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DR GO; GO:0005859; C:muscle myosin; TAS.

DR GO; GO:0008307; F:structural constituent of

InterPro; IPR000048; IQ region.

DR InterPro; IPR001609; myosin head.

DR InterPro; IPR004009; Myosin N.

IR InterPro; IPR002928; Myosin tail.

R Pfam; PF00612; IQ; 1.

R Pfam; PF00063; myosin head; 1.

Pfam; PF00736; Myosin N; 1

Pfam; PF00736; Myosin N; 1
 PIR; 138055; 138055.
HSSP; P13538; 2MYS.
Genew; HGNC:7578; MYH8.
                                                                                                                                                                                                                   EMBL; M36769; AAC17185.1; -.
EMBL; Z38133; CAA86293.1; -.
EMBL; X51592; CAA35941.1; -.
EMBL; AF067143; AAC21557.1;
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95324556; PubMed=7601129;
Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino
Stedman H.H., Rubinstein N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feghali R., Leinwand L.A.;
"Molecular genetic characterization of a human perinatal myosin heavy chain.";
J. Cell Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of a human perinatal myosin heavy-chain transcript.";
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TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 860-1937 FROM N.A. MEDLINE=89234168; PubMed=2715179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90235862; PubMed=1691980;
Bober E., Buchberger-Seidl A., Braun T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Biochem. 230:1001-1006(1995).
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of three developmentally controlled isoforms of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arnold H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 502-1937 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              split further into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characteristic for alpha-helical coiled coils. MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biochem. 189:55-65(1990)
PR00193; MYOSINHEAVY.
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                                                                                                                                of muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmentally regulated
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NP_BIND
DOMAIN
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SMART; SM00242; MS; 1.
PROSITE; PSS0096; NSc; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Myosin; Muscle protein; Moltigene family; Calmodulin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                     517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 QANISGRGRALSRKYDNNFVAPPPVSRPPLEGGWNWQARGGSAQHTAVQEFPDVEDDVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                           HRELAEMGLDRIAWGQKRSMFSGGVRQL-----YGFLATKQDLDIFNQHSQGK-
                                                                                                                                                     EDNRIVRQRTKMQHEQNREEMDAH--DRFFMDSIK-----QIH------
                           KKKLENDVSQL----QSEVEEVIQESRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERM
                                                                           LKEQLAIVERRANLLQABIEELWATLEQTERSRKIAEQELLDASERVQLLHTQNTSLINT
                                                                                                                                                                                                                              QQEISDL-TEQIAEGGKQ-----IHELEKIKKQVEQEKCEIQAALEEAEASLEHEEGKI 1561
                                                                                                                                                                                                                                                                              QRNFDKVLSEWKQKYEETQAELEASQKESRSLSTELFKVKNVYEESLDQLETLRRENKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASEEEND-SDALDDS--DDDLASDDYDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQIN
  KKRHHEEI FDLEKEFDEALEQLMYKHG
                                                    CRKRAEEVSSFIEFQEKEMEEFVEE-----
                                                                                                                            SRNDALRVKKKMEGDLNEMEIQLNHANRLAAESLRNYRNTQGILKETQLHLDDALRGQED
                                                                                                                                                                              LRIQLELNQVKSEVDRKIAEKDEEIDQL-----KRN-HTRVVETMQSTLDAEIR---
                                                                                                                                                                                                     TRIKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAKVLEESLEIMSEKLRRTA
                                                                                                                                                                                                                                                                                                                                                                                                         EPOROWHCPACONGPGAIDWYNLHPLLAHARTKGARRVKLHRELAEVLEKDLOMRGASVI
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                                                                                                                                                                                                                                                                                                                                                       PCGEIYGQWKGLGEDEKDYEIVWPPMVIIMNT--RLDKDDNDKWLGMG------
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19.3%;
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A -> Q (IN REF. 1 AND 4).

M -> Q (IN REF. 3).

M -> H (IN REF. 1 AND 4).

MC -> DGG (IN REF. 3).

E -> G (IN REF. 1 AND 4).

K -> Q (IN REF. 1 AND 4).

K -> Q (IN REF. 1 AND 4).

K -> D (IN REF. 1 AND 4).

EN -> AH (IN REF. 1 AND 4).

B -> D (IN REF. 1 AND 4).

B -> D (IN REF. 1 AND 4).

B -> D (IN REF. 1 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                 -----RTKYETDAIQRTEELEEAKKKLAQR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; A3EE2D151792E9E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 174; DB 1;
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIN-BINDING ACTIN-BINDING
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   619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SKQASTQQIEELKHQLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1937;
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                                                    ---REMLIKDQEKK--MEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 206;
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                            1785
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Matches 130
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067124;
16-0CT-2001
                                                                                                                                                                                                                                                                    Pfam; Pr0433; DCC; 1.
TIGRAM6; TIGR00618; Sbcc; 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete DNA repair; Hydrolase; ATP (BY SIMILARITY).
NP BIND 32 39 ATP (BY SIMILARITY).
DOMAIN 160 826 COILED COIL (POTENTIAL).
DOMAIN 078 AA: 115897 MW; 9B0F2BF51ADD1151 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aquifex aeolicus.
Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAD50 OR AQ 1006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaaserland T.,
Graham D.E., Overbeek R., Snead M.A., Ke
Feldman R.A., Short J.M., Olson G.J., Sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00449; -; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A70387; A70387
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000718; AAC07092.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                   interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Forms a complex with mrell (By similarity). SIMILARITY: Belongs to the SMC family. RAD50 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome
               236
                                                                                                                                                                                                                         130;
                                                                                                                                                                                                                                       Similarity
                                            IDKKLTELKVRKNKLTKELAVLKDELSFAQEELNRIEAEKEKFKEEKEREKE------
                                                                                                     LROELKKAEEKDSLERELSOVVTKLKELENLEKEVEKLREKLEFSRKVAPYVPIAKRIEE
                                                                                                                                 ASEEENDSDALDDSDDDLAS-----DDYDSDVS---QKSHGSRK------
                                                                                                                                                                               NLEGKREALKKEYELLKDYT---PTKKEVLE-----
               GAIDWYNLHPLLAHARTKGARRVKLHRELAEVLEKDLOMRGASVIPCGEIYGOWKGLGED
                                                                                                                                                                                                                                                                                                                                                                     IPR003439; ABC transporter.
IPR007523; DUF498.
IPR004592; SbcC.
IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Creat
(Rel. 40, Last
(Rel. 41, Last
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                                                                                                                                                                                                                                     19.6%;
                                                                        QNKWFKKFFGSLDSLSI -- EQIN---
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Olson G.J., Swanson R.V.;
he hyperthermophilic bacterium
                                                                                                                                                                                                                         107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
annotation update)
break repair rad50
                                                                                                                                                                                                                                       Score 173.5; DB Pred. No. 0.062;
                                                                                                                                                                                                                          Mismatches
978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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ller M., Auj
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                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                ----KTLKNLEEELKELKETEEK 225
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MBL outstation -
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P02562;
21-JUL-1986
01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RABIT
                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolas
                                                                               Maeda K., Sczakiel G., Wittinghofer A.; "Characterization of CDNA coding for the portion of a rabbit fast skeletal muscle Eur. J. Biochem. 167:97-102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence up
15-WAR-2004 (Rel. 43, Last annotation
Myosin heavy chain, skeletal muscle (F
                                                                                                                                      SEQUENCE OF 409-1084 FROM N.A.
MEDLINE=87304245; PubMed=3305014;
                                                                                                                                                                                         region
                                                                                                                                                                                                        Lu R.C., Wong A.;
"The amino acid sequence and
                                                                                                                                                                                                                                SEQUENCE OF 259-428.
MEDLINE=85131142; PubMed=3972832;
                                                                                                                                                                                                                                                                                       myosin."
                                                                                                                                                                                                                                                                                                    Capony J.-P., Elzinga M.; "The amino acid sequence of A 34,000
                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-258.
                                                                                                                                                                                                                                                                          вторнув.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
                                                                                                                                                                              Biol.
                                                                                                                                                                                                                    R.C.,
 FUNCTION: Muscle contraction.
SUBUNIT: Muscle myosin is a hexameric protein that consist heavy chain subunits (MHC), 2 alkali light chain subunits and 2 regulatory light chain subunits (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: The rodlike tail sequence is highly repetitive, sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VELYLGDKEAELERKIKEFEESFQSLKLKKSEIEEKLKEYEGIRELSDIKGEYESVKTQL
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                                                                                                                                                                                         myosin
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                                                                                                                                                                              in subfragment 2.";
260:3456-3461(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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ATP-binding; Mul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             split further into 2 globular subfragments (S1) and 1 rod-shaped
subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils and an ach myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A02985; A02985.
A05280; A05280.
S00084; S00084.
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 ASERVQLLHTQN---
                                                                                                                                                                     TGYLEA----ERLHRELAEMGLDRIAWG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAQRLQDAEEHVEAVNS-----KCASLEKTKQRLQNEAEDL-----MIDVERSN
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                                                                                                                                                 RVVESMQSTLDAEIR---SRNDALRIKKKMEGDLNEMEIQLNHANRQAAEAIKNLRNTQG
                                                                                                                                                                                                                                                             LATKODLDI FNOHSOGK-TRLKFELKSYQEMVVKELRQISEDNOQLNYFKNKLSKQNKHA
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-TSLINTKKKLETDISQI----QGEMEDIVQEARNAEEKAKKAITDA
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V -> L.
E -> D.
S -> G.
K -> R.
MW; 229(
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Pred. No. 0.
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.074;
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RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bardy C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Conroy D., Coxby N.R., Fleming K., French L., Garner A.A.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Hail R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA McClay J., Mclaren S., McMurray A.A., Mine S.A., Mortimore B.J.,
RA McClay J., Mclaren S., McMurray A.A., Nine S.A., Mortimore B.J.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Vaudin M., Wallim S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Vaudin M., Wallims S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Berkey S., Kogers J., Shimizu N.,
RA Wright C.L., Hubbard T., Berkey S., Kogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
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MEDLINE=21067080; PubMed=11148140;

MEDLINE=21067080; PubMed=11148140;

Medley Q.G., Streuli M.;

Seipel K., O'Brien S.P., Iannotti E., Medley Q.G., Streuli M.;

"Tara, a novel F-actin binding protein, associates with the Tr

"Tara, a novel F-actin binding protein, associates with the Tr
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(9412D6; 094797; Q95DW1; Q95T77; Q95T17; Q95Y9.

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

TRIO and F-actin binding protein (Protein Tar)

repeat on actin) (HRIHFB2122).

TRIOBP OR TARA, OR KIAA1662.
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"Construction of expression-ready cDNA
curation of 330 KIAA cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20057165; PubMed=10591208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21156230; PubMed=11258795;
Hirosawa M., Nagase T., Murahashi Y.,
"Identification of novel transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22158633; PubMed=12168954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Primates;
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A clones
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Q9BY98;
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r KIAA genes:
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RA Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Pulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
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RY The DNA sequence of human chromosome 22.";
RI Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., And Jiatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., RA Bosak S.F., Loquellano N.A., Deters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Warny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A., Rah Fahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A., Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Schesh J.E., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Schmarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Thuman and mouse cDNA sequences.", Typoc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 340-563 FROM N.A., AND TISSUE-Fetal brain;
MEDLINE-99068504; PubMed-9853615;
Ueki N., Oda T., Kondo M., Yano K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Selection system for genes encoding nuclear-targeted proteins.";
Nat. Biotechnol. 16:1338-1342(1998).
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                                                                                                                       This
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3 O W
                                                                                                                                                                                                                                                                                                                                                                                                                                            PUNCTION: May regulate actin cytoskeletal organization, cell spreading and cell contraction by directly binding and stabil: spreading and cell contraction by directly binding and stabil: filamentous F-actin. The localized formation of TARA and TRIO complexes coordinates the amount of F-actin present in stress fibers. May also serve as a linker protein to recruit proteins required for F-actin formation and turnover. SUBUNIT: Binds to TRIO and F-actin. May also interact with mycrosum.
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                               for genes encoding nuclear-targeted protein. SIMILARITY: Contains 1 PH domain. CAUTION: Ref.6 sequence differs from that sh frameshift in position 478.
                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                and placenta.

DOMAIN: Contains at least 2 actin-binding
                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear and
                                                                                                                                                                                                                                                             MISCELLANEOUS: Has
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CIFICITY: Widely e
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                                                                                                                                                                                                                                                                been identified in Ref.6
                                                                                                                                                                                                    differs from that shown
                                                                                                                                                                                                                                                                                                                                                              expressed. Highly expressed in heart
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REMBL; AB051449; BAB33332.2; ALT_INIT.

REMBL; Z83844; CAB42898.3; -.

REMBL; BC003618; AAH03618.1; -.

REMBL; BC00378; AAH04303.1; ALT_INIT.

REMBL; BC004303; AAH04303.1; ALT_FRAME.

REMBL; BC004303; AAH04308.1; ALT_FRAME.

REMBL; BC001378; AAH13278.1; ALT_FRAME.

REMBL; BC001378; F:actin cytoskeleton; NAS.

REMBL; AB015343; BAA34800.1; ALT_FRAME.

REMBL; AB051844; BAB33332.2; ALT_INIT.

REMBL; AB051844; BAB33332.2; ALT_INIT.

REMBL; AB051449; BAB34301.1; ALT_INIT.

REMBL; AB051449; BAB43801.1; ALT_INIT.

REMBL; AB051449; BAB43800.1; ALT_INIT.

REMBL; BC0036181; ALT_INIT.

REMBL; BC0036181; ALT_INIT.

REMBL; AB04144900.1; ALT_INIT.

REMBL; ALT_INIT.

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MT -> RR (IN REF. 2 AND 3).

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S -> T (IN REF. 1).

M -> I (IN REF. 5; AAH04303).

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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Intermediate filament-associated protein that associates in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipeptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even anchor the cell envelope to the KIF network. It may be involved in its own calcium-dependent postsynthetic processing during remning differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probably con
SIMILARITY:
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: Substrate of transglutaminase. Some 200 arginines probably converted to citrullines by peptidylarginine c SIMILARITY: In the N-terminal section; belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calcium-binding domains. Domains 2-4, 6, and 8 are almost entirel alpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domains 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: Expressed during late differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homodimer (Probable).
TISSUE SPECIFICITY: Found in the hard keratinizing tissues such the inner root sheath (IRS) of hair follicles and medulla, and the filiform papillae of dorsal tongue epithelium (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: Consists of nine domains. Domain 1 contains two
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                                                                                                                                                                                                                                                                                                                                                                                                                                       S28589; S28589.
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IPR002048; EF-hand.
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detazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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30, Last sequence up
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                                                                                                                                                                                                                 "Replacement of threonine residues by phosphorylatable heavy chain fragment FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P08799;
01-NOV-1988
MEDLINE=95345066; PubMed=7619795;
                                                               Dictyostelium myosin heavy
FEBS Lett. 227:71-75(1988)
                                                                                                                           Wagle G.,
                                                                                                                                                  MEDLINE=88112226; PubMed=2828113;
                                                                                                                                                                                                                                                                                  Gerisch G.;
                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION SITES,
                                                                                                                                                                                                                                                                                                                                                                                                                                "Conserved protein domains in a myosin Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87092266; PubMed=
Warrick H.M., de Lozanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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                    K-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                        PHOSPHORYLATION SITES
                                                                                                                                                                                                                                                                                                  Lueck-Vielmeter D.,
                                                                                                                                                                                                                                                                                                                           MEDLINE=90353583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                         Wagle G., Noegel A., Scheel J., Gerisc
Phosphorylation of threonine residues
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annotation update)
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Pred. No. 0.:
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                                                                                                                              Gerisch
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                                                                                                                                                                                                                                                                                                  Wippler J.,
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X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE=96206189; PubMed=8611530;
Smith C.A., Rayment 1.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II)-pyrophosphate complex of the truncated head of Dictyostelium discoideum myosin to 2.7-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rayment I.; "X-ray Biructures of the myosin motor domain of Dictyostelium "X-ray structures of the myosin motor domain of Dictyostelium discoideum complexed with MgADP.BeFx and MgADP.AlF4-."; Biochemistry 34:8960-8972 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fisher A.J.,
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MEDLINE=97452580; PubMed=9305951;
Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
nx-ray structures of the MgADP, MgATPgammaS, and MgAMPPNP complexes
of the Dictyostelium discoideum myosin motor domain.";
of the Dictyostelium discoideum myosin motor domain.";
Biochemistry 36:11619-11628(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 34:8973-8981(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95345067; PubMed=7619796;
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Biochemistry 35:5404-5417(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "X-ray structure of the magnesium(II).ADP.vanadate complex of the Dictyostelium discoideum myosin motor domain to 1.9-A resolution.";
                                                                                                                                                                                                                  This
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                                                                                                                     or send an
                                                                                                                                         entities requires a
                                                                                                                                                                                                   between
                                                                                                                                                                                                                                           DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils. Characteristic for alpha-helical coiled coils. The sequence of the actin-activated Affase activity.

MISCELLANEOUS: Dictyostelium myosin II has no K(2)EDTA AFFase activity, perhaps correlated with the absence of a Cys at the SH-1 position (688).

SIMILARITY: Contains 1 myosin-like globular head domain.

SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can be further split into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE
A26655; A26655.

1MMA; O3-DEC-97.

1MMD; 17-AUG-96.

1MMG; O3-DEC-97.

1MMN; O3-DEC-97.

1MND; 17-AUG-96.
                                                                                                                                                                                      European
                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through neen the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content by non-profit institutions as long as its content by non-profit institutions. Usage by and field and this statement is not removed. Usage by and field and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762
                                                                                         M14628; AAA33227.1;
                                                                                                                       equires a license agreement (S email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00063; myosin
Pfam; PF02736; Myosin
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Myosin; Coiled coil
Calmodulin-binding;
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1D0Y;
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SM00242;
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23-DEC-96.
28-JAN-98.
20-DEC-00.
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IPR001609; myosin_head.
IPR004009; Myosin_N.
IPR008989; Myosin_S1_N.
                                                 myosin head; 1.
Myosin N; 1.
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                     Actin-binding; ATP-binding;
Methylation; Phosphorylation.
MYOSIN HEAD-LIKE.
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ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING.
PHOSPHORYLATION (B:
PHOSPHORYLATION (B:
PHOSPHORYLATION (B:
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        MYH4 RABIT STANDARD; PRT; 1938 AA (28641; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Myosin heavy chain, skeletal muscle, juveni
                                                                               RABIT
 Oryctolagus cuniculus (Rabbit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 DVEDDVDNASEEENDSDALDDSDDDLAS--DD----YDSDVSQKSHGSRKQNKWFKKFFG
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                                                                                                                           IKRLNEELSELRSVLEEADER 1473
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            juvenile
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QEFPDVEDDVDNASEEEND-----SDALDDS--DDDLASDDYDSDVSQKSHGSRKQNK--

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Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                             муовіп;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32574; AAA7419
PIR; A59293; A59293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wittinghofer A.;
"Isolation, sequencing of myosin heavy chain cDNA from to be a sequencing of myosin heavy chain cDNA from to be a sequence of S-1 fragment."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maeda K., Hostinova Wittinghofer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=New Zealand
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and 2 regulatory light chain subunits (MLC-2).

SUBCELULIAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.

MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).

SIMILARITY: Contains 1 myosin-like globular head domain.

SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Muscle myosin is a hexameric protein that consist heavy chain subunits (MEC), 2 alkali light chain subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Muscle contraction
121;
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                         Similarity
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protein; Coiled coil;
iding; ATP-binding; Met
MYOSIN
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                         5.1%;
21.1%;
                                                                                                223064
                                                                                                                    COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (MONO-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).
                                                                                             MW; D8A8A2EC5B182626
                      Score 169;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                           coil; Thick filament; Actin-binding;
g; Methylation; Multigene family.
YOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                         DB 1;
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work. It may be involved in processing during terminal

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ID TRHY HUMAN

AC 007283;
DT 01-0CT-1994
DT 115-MAR-2004
DT 15-MAR-2004
DT 10-MAR-2004
RN THH OR TRHY
OS HOMO sapien
OC Mammalia; B
OX NCBI TAXID=
RN (1]
RN SEQUENCE FR
RX MEDLINE=932
RA Steinert P.;
RA STEINESCOPE PR
RY MEDLINE=932
RY 11-MAR-1992
RY SEQUENCE OF
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RA O'Keefe E.J
RT STICHOMPAIL
RT Epidermis:"
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CC -1- FUNCTIO
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01-OCT-1994
01-OCT-1994
15-MAR-2004
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-93280194; PubMed=7685034;
Nee S.-C., Kim I.-G., Marekov L.N
                                                                                                                   SEQUENCE OF 1731-1898 FROM N.A., AND CHARACTERIZATION.
MEDLINE=93315897; PubMed=7686953;
O'Keefe E.J., Hamilton E.H., Lee S.-C., Steinert P.M.;
"Trichohyalin: a structural protein of hair, tongue, n
                                                                                                                                                                                                envelope precursor, linking) protein."; J. Biol. Chem. 268:1
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                             Trichohyalin.
THH OR TRHY OR THE
                                                                                                                                                                                                                           "The structure of human trichohyalin. Pofunctional EF-hand-like calcium-binding envelope precursor, and an intermediate
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                e S.-C.,
   FUNCTION: Intermediate filament-associated protein that associated in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipeptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even
                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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                                                                                            Dermatol.
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Primates;
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                                                                                            101:658-718(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation
                                                                                                                                                                   FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
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                                                                                                                                                                     CHARACTERIZATION
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              Pfam; PF00036; efhand; 1.

Pfam; PF01023; S 100; 1.

ProDom; PD003407; CaBP S100;

PROSITE; PS00018; EF HAND;

PROSITE; PS00303; S100_CABP
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GO; GO:0005599; F:calcium ion bindi:
InterPro; IPR001751; CaBP_5100.
InterPro; IPR002048; EF-hand.
InterPro; IPR002047; Spectrin.
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its own calcium-dependent p
differentiation.
SUBUNIT: Monomer (Probable)
TISSUE SPECIFICITY: Found i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. Th
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Substrate of transglutaminase. Some 200 arginines probably converted to citrullines by peptidylarginine similarity: In the N-terminal section; belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium-binding domains. Domains 2-4, 6, and 8 are almost entirely alpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domains 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among the molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Found in the hard keratinizing tissues such the inner root sheath (IRS) of hair follicles and medulla, and the filiform papillae of dorsal tongue epithelium (Probable). DEVELOPMENTAL STAGE: Expressed during late differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 2 EF-hand calcium-binding domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                different species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 email to license@isb-sib.ch).
              4ICB
                                                                                                                                                                                                                                                                                                                                                                                           Calcium-b
              license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                      S100;
                                                                                                                                                                                                                                                                                                                                                                                                             CABP;
                                                                                                                                                                                                                                                                                                                                                                                        inding; Repeat; Citrullination.
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EF-HAND 2 (HIGH AFFINITY) (PO

6 X 13 AA TANDEM REPEATS OF

R-R-E-Q-E-E-R-R-E-Q-Q-L.

1-1 (APPROXIMATE).

1-2 (APPROXIMATE).
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(See http://www.isb-sib.
                                             APPROXIMATE TANDEM REPEATS.
TANDEM REPEATS.
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MYHD HUMAN
D171--

Q9UXX3; 095252;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
1--in heavy chain, skeletal muscle, extraocular (MyHC-eo)
--in heavy chain, skeletal muscle, extraocular (MyHC-eo)
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                TISSUE-Extraocular muscle;
MEDLINE-99318869; PubMed=10388558;
Weiss A., Schiaffino S., Leinwand L.A.;
"Comparative sequence analysis of the conheavy chain family: implications for fur J. Mol. Biol. 290:61-75(1999).
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SEQUENCE OF 1917-1938 FROM N.A.
                                                                                               SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID=9606;
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Q -> K (I
V -> G (I
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                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Winters L.M., Briggs M.M., Schachat F.;
"The human extraocular muscle myosin heavy chain
the cluster of fast and developmental myosin gene
Genomics 54:188-189(1998)
                                                                                                                                                                                                                                                Myosin; Muscle prote Calmodulin-binding;
                                                                                                                                                                                                                                                                                                               PRINTS; PR00193; MYOSTNHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000048; IQ region.
InterPro; IPR001609; myösin head.
InterPro; IPR004009; Myosin N.
InterPro; IPR002928; Myosin tail.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0003779; F:actin binding; NAS.
GO:0005524; F:ATP binding; NAS.
GO:0005516; F:calmodulin binding; NAS.
GO:0003776; F:muscle motor activity; TAS.
GO:0006936; P:muscle contraction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 603487; -. GO:0005859; C:muscle myosin; TAS. GO:0003779; F:actin binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2). SUBCELLULAR LOCATION: Thick filaments of the myofibrils. DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils. MISCELLANEOUS: Each myosin heavy chain can be split into 1 light mercomyosin (LMM) and 1 heavy mercomyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 myosin-like SIMILARITY: Contains 1 IQ domain.
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SUBUNIT: Muscle myosin is a h
                                                     115 SRKYD-----NNFVAPPPVSRPPLEGGWNWQARGGSAQHTAVQEFPDVEDDVDNASEEE
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PF00063; myosin_head; 1.

PF02736; Myosin_N; 1.

PF01576; Myosin_tail; 1.
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MYOSIN HEAD-LIKE.
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Pred. No. 0.3
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ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hyaluronan mediated motility receptor (Intracellular hyaluronic acion binding protein) (Receptor for hyaluronan-mediated motility) (CD168
                                                                                                                                                                                                                                                                                                                                                       075330; Q92767;
30-MAY-2000 (Re
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                                                                                                                           MEDLINE-90264864; PubMed-9601098;
Assmann V., Marshall J.F., Fieber C.,
"The human hyaluronan receptor RHAMM ;
protein in breast cancer cells.";
J. Cell Sci. 111:1685-1694(1998).
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                             HMMR OR IHABP OR RHAMM.
                                                                                                                                                                                                                                                                                                    binding protein)
MEDLINE=97045829; PubMed=8890751;
Wang C., Entwistle J., Hou G., Li Q., T
"The characterization of a human RHAMM hyaluronan-binding domains.";
Gene 174:299-306(1996).
-I- FUNCTION: Involved in cell motility
HMMR, the phosphorylation of a numb
                                                                                                                                                                                          TISSUE=Breast carcinoma;
                                                                                                                                                                                                    SEQUENCE FROM N.A., ALTERNATIVE
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Best Local
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DOMAIN 635
DOMAIN 657
CARBOHYD 133
CARBOHYD 477
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CONFLICT
CONFLICT
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CARBOHYD
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                                                                                                                                                                                                                                                                                           SIDSLSIEQINEPOROWHCPAÇONGPGAIDWYNLHPLLAHARTKGARRVKLHRELAEVL-
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                                                                                                                                        AEMGLDRIAWGOKRSWFSGGVRQLYGFLATKQDLDIFNQ-----HSQGK------
                                                                                                                                                                                                                                           -EKDLOM-RGASVIPCGEIYGQWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWLGMG
                                       SLEIMSEK------LRRTAEDNRIVRQRTKMQHEQNREEMDAHDRFFMDSIKQIHE
                                                                 SIEKEKIDEKSETEKLLEYIEEISCASDQVEKYKLDIAQLEENIKEKNDEILSLKQSLEE
                                                                                       --TRLKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAK------VLEE
                                                                                                                  RILSLELMKLRNKRE-----TKMRGMMAKQEGMEMKLQVTQRSLEESQGKIAQLEGKLV
                                                                                                                                                                   IQDLETELEKWEARLNAALREKTSLS-ANNATLEKQLIELTRTNELLKSKFSENGNQKNL
                 NIVILSKQVEDLNVKCQLLEKEKEDH -- VNRNREHNENLNAEMQNLKQKFILE--QQERE
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75
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332
                                                                                                                                                                                                                                                                                                                                                                         84031 MW;
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)%; Pred. No. 0.12;
100; Mismatches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=075330-2; Sequence=VSP 004286; -i- TISSUE SPECIFICITY: Expressed in breas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        focal adhesion kinase occurs. May also be involved in cellular transformation and metastasis formation, and in regulating extracellular-regulated kinase (ERK) activity.
SUBCULTIAN LOCATION: Cell surface and cytoplasmic (By
                                                                                                                                                                                                                                                                                             normal breast tissue.
DATABASE: NAME=PROW; NOTE=PROW 2:76-84(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/802868666_g.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=075330-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                       breast
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N-LINKED (GLCNAC. .) (E N-LINKED (GLCNAC. .) (E N-LINKED (GLCNAC. .) (I N-LINKED (GLCNAC. .) (I N-GRACHE (GLCNAC. .) (I N-GRAC Missing (in isoform B).
/FTIdaVSP 004286.
K -> KK (IN REF 2).
S -> R (IN REF 2).
E -> D (IN REF 2).
K -> T (IN REF 2).
K -> T (IN REF 2).
C -> R (IN REF 2). splicing; Repeat; Glycoprotein; Ant HYALURONIC ACID-BINDING (POTENTIAL) HYALURONIC ACID-BINDING (POTENTIAL) N-LINKED (GLCMAC. .) (POTENTIAL) EA68AD6D2A626926 멂 1; Length 724; CRC64; (POTENTIAL).
(POTENTIAL). (POTENTIAL) Antigen.

186;

Indels

102;

Gaps

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376 104 326 55 268

163

467 217 420

Search completed: Job time : 22 secs	Db	Ş	Ъ	&
omple: : 22	394	559	334	518
Search completed: April 6, 2004, 19:33:55 Job time : 22 secs	394 QAERLVKQLEEEAKSRAEELKLLEEKLKGKEAELEKSSAAHTQATLLLQEKYDSMVQSL 452	559 EVSSFIEFQEKEMEEFVEEREMLIKDQEKKMEDMKKRHHEEIFDLEKEFDEALEQL 614	334 KLQQKELQIDSLLQQEKELSSSLHQKLCSFQEEMVKEKNLFEEELKQTLDELDKLQQKEE 393	518 RRDAKEENFEMLOOQERAKVVGQQQQNINPSSNDDCRKRAE 558

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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Gapop 10.0 , Gapext 0.5
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3313
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sp_organelle:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_vriclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	IJ	4	u	2	_	Result No.
189.5	190	190	192	192	194.5	198	203	208	211	215.5	233.5	242	548.5	778	3313	Score
5.7	5.7	5.7	5. 8	5.8	5.9	6.0	6.1	6.3	6.4	6.5	7.0	7.3	16.6	23.5	100.0	Query Match Length
638	639	635	2760	634	447	1036	628	1003	634	629	644	647	170	304	625	Length
10	10	10	5	10	10	12	10	12	10	10	10	10	10	10	10	BB
Q9LHB1	Q8W563	Q9C7B0	Q815Y2	Q9S9P3	Q8H8B2	Q9DUM3	Q8LSJ9	Q91LX9	Q9SAI1	Q9SBW2	Q9SMN2	Q8VZ79	Q7XYE6	Q7XY17	O9LDX1	ID
Q9lhb1 arabidopsis	Q8w563 triticum mo	Q9c7b0 arabidopsis	Q8i5y2 plasmodium	Q9s9p3 arabidopsis	Q8h8b2 oryza sativ	Q9dum3 kaposi′s sa		Q91lx9 kaposi's sa	Q9sail arabidopsis	Q9sbw2 oryza sativ	Q9smn2 arabidopsis	Q8vz79 arabidopsis	Q7xye6 triticum ae	Q7xy17 triticum ae	Q9ldx1 arabidopsis	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
171.5	171.5	171.5	172	172.5	172.5	172.5	173	174	174	175.5	176	176	177 "	177	178	178	178.5	179	179.5	180	180.5	181	183	183.5	186	186	186.5	187
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097291 plasmodium	Q9tv61 sus scrofa	mus mu		Q9srd5 arabidopsis	066878 aquifex aeo		O45420 caenorhabdi	CO.	Q90y37 brachydanio		Q8iif6 plasmodium		Q9qr71 kaposi′s sa	Q869r0 dictyosteli	Q9u0s7 mytilus gal	Q9u0s5 mytilus gal		Q8i3p4 plasmodium	ъ	O23064 arabidopsis				arabid	gallus		arabio	Q9ax36 oryza sativ

ALIGNMENTS

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Query Match
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Matches 629
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EMBL; B7239719; AAF73960.1; ---
EMBL; BT002944; AA022757.1; ---
EMBL; BT004380; AA042374.1; ---
EMBL; BT004380; AA042374.1; ---
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SEQUENCE FROM N.A., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.
Yamada K., Chan M.M., Chang C., Toriumi M., Wong C., Wu H.C.,
Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Yu G., Yuan S., Carninci P., Chen H., Kim C.J., Narusaka M.,
Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Ecker
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InterPro; IPR005381; zf.
Pfam; PF03468; XS; 1.
Pfam; PF03470; zf.XS; 1.
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                                                                TRLKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAKVLBESLEIMSEKLRRTA
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                                | OQQNINPSSNDDCRKRABEVSSF1EFQEKEMEEFVEEREMLIKDQEKKMEDMKKRHHEEI
FDLEKEFDEALEQLMYKHGLHNEDD
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Q7XY17;
01-OCT-2003
01-OCT-2003
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STRAIN-CV. PH 82-2-2;
Zhao X., Li Q., Zhang X.;
Zhao X., Li Q., Zhang X.;
Taolation and expression of a new kind of gene involve unbryogenesis in Triticum aestivum L.";
embryogenesis in Triticum aestivum L.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF542974; AAA980862.1;
EMBL, AF542974; AAA980862.1;
SEQUENCE 304 AA; 35958 MW; 89980215A9584208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               викатуота; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
SEQUENCE FROM N.A.

STRAIN=cv. PH 82-2-2;
Li J.R., Wang F., Li Q.Z., Zhang X.S.;
"Gene isolation and expression of a new Zn-finger.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF469493; AAP80610.1; -.

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                                                                                                                                                                Q7XYE6;
Q7XYE6;
01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                          HOTR (Fragment).
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Triticeae; Triticum.
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; Pred. No. 9.7e
58; Mismatches
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Last sequence update)
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Matches 101;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Mirana...
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.,
Chhmitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Sakurai T., Theologis A., Davis R.W.;
Ecker J., Theologis A., Davis R.W.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, B7000136; AAN15455.1; -.

EMBL, B7000136; AAN15455.1; -.
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Q8VZ79;
01-MAR-2002
01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                           Hypothetical
SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. AT3G48670.
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PF03468; XS; 1.
PF03470; zf-XS; 1.
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; IPR005380; XS.
; IPR005381; zf.
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                                                                                                                                                         LASDDYDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQINEPQRQWHCPACONGPGAIDW
YK--DLLQHASGVGNSNSDKRSAKEKASHLALVKYLQQDLADSASEAEPSSKRQKNGNPI
                                                  YNLHPLLAHARTKG
                                                                                                       LSSDDEDSDISES----EMDEYGDKMYLNLKGGKLKVRLSPQ-AFICPYCPNKKKTSFQ
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647 AA; 74824 MW;
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Pred. No. 2.2e
31; Mismatches
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Last annotation updat
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                                                                                                                                                                                                                                        Score 242; DB 10;
Pred. No. 2.3e-06;
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36;
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PIR;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL, AL133315; CAB62356.1; -.
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Artiguenave F., Saurin W., Weissenbach
Mayer K.F.X., Quetier F., Salanoubat M.
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rPro; IPR005381; zf.
; PF03469; XH; 1.
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; PF03470; zf-XS; 1.
                                                                  181
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Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki T., Matsumoto T., Yamamoto
"Oryza sativa nipponbare(GA3) gen
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2 (TrEMBLrel. 22, Last an
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; XS; 1.
; zf-XS; 1.
9 AA; 72715 |
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21.1%;
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annotation update)
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     215.5; DB 1
No. 8.5e-05;
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Theologis A.;
Submitted (DEC-1999) to th
EMBL; ACO11713; AAF14667.1
PIR; E96840; E96840.
InterPro; IPR005379; XH.
InterPro; IPR005380; XS.
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Q9SAII;
O1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                              STRAIN-cv. Columbia; Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S., Lee J.M., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S., Lee J.M., Gorbartz J.R., Liu K., Sakano H., Koo T., Pham P., Vays Howng B., Chin C., Choi B., Chiou J., Altafi H., Brooks S., Conm L., Conway A., Hansen N., Johnson-Hopson C., Khan S., Ki Conn L., Conway A., Palm C., Shinn Bounga G., Davis R.W. Ecker J.R., Federspiel N.A., Theologis A.; "Arabidopsis thaliana chromosome 1 BAC F23A5 sequence.";
                                                                                                                                                      STRAIN=cv.
                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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GLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKYEALRARHSYGPQG
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QEKMDELDAMESLNQTLVIKERKSNTEMQDARKELENGLLDL
                                        QEK--EMESFVEEREMLIKDQEK---KMEDMKKRHHEEIFDL
                                                                                                                       FMDSIKQIHERRDAKEENFEMLQQQERAKVVGQQQQNINPSSNDDCRK-RAEEVSSFIEF
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                                                                                                                                                                                                                                                             SLEKMMGQREQLLQKYNEEIRKMQQLAQRHSQKIIDENQKLRSELESKMSELNTRSKELD
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                                                                                   VKKILKLEQQVDAKQK-LELDIQQLKGKLEVMKHM--
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis. Last sequence update)
Last annotation update) Created) PRT; ₽ rosids;

EMBL/GenBank/DDBJ databases

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Khan S., Kim Davis R.W.,

Vaysberg S., Chao Q

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Best Local Sim
Matches 107;
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Q91LX9;
01-DEC-2001
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Pfam; PF03
Pfam; PF03
Pfam; PF03
                                                                                                                                                                                    Kaposi's sarcoma-associated herpesvirus (KSHV) (Human Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
J. Virol. 75:7882-7892(2001).
EMBL; AF360120; AAK50002.1; -.
InterPro; IPR002017; Spectrin.
InterPro; IPR002033; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
SEQUENCE 1003 AA; 115517 MW;
                                                                                        Garber A.C., Shu M.A., Hu J., Renne R.;
"Dna binding and modulation of gene expression by the latency-associated nuclear antigen of Kaposi's sarcoma-associated
                                                                                                                                                                                                                                  ORF73
                                                                                                                                                                                                                                            01-DEC-2001
01-OCT-2003
                                                                                                                                   MEDLINE=21376412; PubMed=11483733;
                                                                                                                                              SEQUENCE FROM N.A.
                                                                              erpesvirus.";
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PF03468;
PF03470;
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03469; XH; 1.
03468; XS; 1.
03470; zf-XS; 1.
634 AA; 74293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRGASVIPCGEIYGQWKGLGEDEKDYEIVWPPMVIIMVTRLDKDDNDKWLGMGNQELLEY
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(TrEMBLrel. 19, Last seq
(TrEMBLrel. 25, Last ann
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Pred. No. 0.00016;
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  C20C43308B01A0A3
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Best Local S
Matches 91
Interr.; I.ROO5.
InterPro; IPROO5.
InterPro; IPROO5.
Pfam; PFO3468; XK; 1.
PFam; PFO3468; XS; 1.
PFO3470; zf-XS; 1
PFO3470; zf-XS; 1
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01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-line LH82;
MEDLINE-21980573; PubMed=11959909;
MEDLINE-21980573; PubMed H., Yandeau M., Nikolau
                                                                                                                                                                                                                                                                       "From the Cover: Molecular characterization of meiotic across the 140-kb multigenic al-sh2 interval of maize." Proc. Natl. Acad. Sci. U.S.A. 99:6157-6162(2002). EMBL; AF434193; AAM22636.1; -.
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                                                                                                                                                                     InterPro; IPR005379; XH.
InterPro; IPR005380; XS.
InterPro; IPR005381; zf.
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Pred. No. 0.00043;
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Matches 87
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Latent nuclear antigen (Fragment).
Kaposi's sarcoma-associated herpesvirus (KSHV) (Human Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
UCBI TaxID=37296;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDIINE=21165304; PubMed=11264383;

MEDIINE=21165304; PubMed=11264383;

MEDIINE=21165304; PubMed=11264383;

MICOLAS J.C., Marechal V.;

Piolot T., Tramier M., Coppey M., Nicolas J.C., Marechal V.;

Piolot T., Tramier M., Coppey M., Nicolas J.C., Marechal V.;

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      6.0%; Score 198; DB 12;
17.9%; Pred. No. 0.0018;
tive 106; Mismatches 222;
                                                                                                                                     119328 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
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Pred. No. 0.00047;
6; Mismatches 176
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Best Local S
Matches 62
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SEQUENCE FROM N.A.

Wing R.A., Yu Y., Soderlund C
Currie J., Collura K.;

"Rice Genomic Sequence.";

submitted (SEP-2002) to the El
EMBL; AC099401, AAN06846.1;

InterPro; IPR005380; XS.

pfam; PF03468; XS; 1.
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. OJ1134F05.17.
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                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 447 AA; 4
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                                           GEIYGQWKGLGEDEKDYE----
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(TrEMBLrel.
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23, Last sequence update)
24, Last annotation update)
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; Pred. No. 0.00098;
36; Mismatches 76;
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Matches 98
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Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Lenz C., Pham P.,
Liu S.X., Chin C., Chiou J., Choi E., Chung M., Gonzalez A.,
Toriumi M., Chin C., Chiou J., Choi E., Chung M., Altafi H., Brooks S.,
Howng B., Koo T., Liu A., Vaysberg M., Altafi H., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC T24DL8 from Arabidopsis thaliana chromosome 1.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9S9P3, PRELIMINARY; PRT; 634 AA.
O9S9P3,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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; PF03470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
DNQQLNYFKNKLS------KQNKHAKVLBESLEIMSEKLRRTAEDNRIVRQRTKMQH
                                                                                                                                                                                                                                                                                                                                                                EPVPRPPVVPPQLDETEPNPHNVYVWPWMGIVVNPL--KEADDKELLLDSAYWLQTLSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IPR005379; XH.
; IPR005380; XS.
; IPR005381; zf.
                                                                                                      ESKAYGWCARADDFESQGPIGEYLSKEGQLRTVSDISQKNVQDRNTVLEELSDMIAMTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                 SVIPCGEIYGQWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWHCPACQNGPGAIDWYNLHPLLAHA-----RTKGARRVKLHRELAEVLEKDLQMRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIGWLHARANQSVGSDNSPLLVETDNRTGEKRRILYGYLAISSDMDELDSDSRKRASLK 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EM----DKKISELGFAGGKSKSLYGKEGHLGLTLIKFANSPAGLKEAERLADFLERQDHG
                                                                                                                                                                                                                                     KPIEVNAFWVEQDSIVGVIAKFNGDWSGFAGATELEKEFETQGSSKKEWTER----
                                                                                                                                                                                                                                                                                               EALRARHSYGPOGHRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGOKRSMFSG-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLRCPFCA-GKKKQD-YKYKELYAHATGVSKGSATRSALQKANHLALAMFLENEL-AGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIAWGOKRSMFSGGV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YTKVPENSKAYQSLLPDLVQASREDLIIWPPTVIIHNTATGRKKDGRAEGLGNK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; XH; 1.
; XS; 1.
; zf-XS; 1.
4 AA; 72635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 192; DB
22.1%; Pred. No. 0.00
cive 80; Mismatches
                                                                                                                                                                    -DIFNOHSOGKTRLKFELKSYQE--MVVKELRQI----SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0071930DED7F41B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ROLYGFLATKODLDIFNOHSOGKTRLK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 10; Length 634; 0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179;
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Query Match
Best Local Simi
Matches 136;
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01-MAR-2003 (TrEMBLrel. 2
Hypothetical protein.
PFL0315C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q815Y2;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gardner M.J., Hail N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 419:498-511(2002).
EMBL; AE014845; AAN36152.1;
Hypothetical protein.
SEQUENCE 2760 AA; 330896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  falciparum."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q815Y2
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                                                                                                                                                                           1622
                                                                                                                                                                                                                                                                                                                                                                          1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEKNVQGGYRPEVEQLVQGLAGTRLASSQDDGGEWEVISKKN--KNKPGNTSGKTWVSQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEIQELKGKLÓVM-KH-LGDDDD 436
                                                                                                                                                                                                                                                                                                                                                                     K-----KKEKKKNNWAMYGRPIVKRONNRNINIKNDLK---KLYSSKSESGF----
-AEVLEKDLOMRGASVIPCGEIYGQ-----WKGLGEDEKDYEIVWPPMVIIMVTRLDKDD 318
                                                                          NSSNNKIVKRTSIKN--NTIDNYNNSTIKKIIHKEONVEDOGYIDLKTKRKLIYDALDEI 1739
                                                                                                                                                                                                                                                                                                                                                                                                                      SNPPRAWGGQQQGRGSNVSGRGNNVSGRGNGNGRGIQANISGRGRALSRKYDNNFVAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEMDVNSKNEREIVQVHNEIKNTN--NKEEEG-----KKKNLLKEKEINDCLNDYINKQ
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                                                                                                                          NEPQRQ-WHCPACQNGPGAIDWYNLHPL--LAH----ARTKGARRVKLHREL-----
                                                                                                                                                                           KENIYENSPFHTYGRPIYEKKSKNPNNYNKIKSTTHNAILKKKRKKTLNKSISINSFTKM
                                                                                                                                                                                                                                                                         -----NDYAFYAERFFEVITGYNSEPDYLSDIDNQAKNEENKNDIIHNNNIIKISKKM 1621
                                                                                                                                                                                                                                                                                                                       VSRPPLEGGWNWQARGGSAQHTAVQEFPDVEDDVDN-ASEEENDSDALDDSD-----DDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 142; Mismatches 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 192; DB 5 19.7%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330896 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (isolate 3D7).
Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23,
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Last annotation updat
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                                                                                                                                                                                                                      ---VSQKSHGSRKQNKWFKKFFGSLDSLSIEQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 142;
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                      RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Ra Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B., Ra Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B., Ra Grismann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B., Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., Ra De Simone V., Choisne N., Artiquenaev F., Robert C., Brottier P., Ra Mincker P., Cattcolico L., Weissenbach J., Saurin W., Quetier F., Ra Wincker P., Cattcolico L., Weissenbach J., Saurin W., Quetier F., Ra Wincker P., Cornek H., Erfle H., Jordan N., Benes V., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Quetier F., Ra Winckelnann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G., Ra Winckelnann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G., Ra Raichelt J., Scharfe M., Pallavicini A., Toppo S., Simionati B., Vezzi A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G., Ra Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Ra Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent D., Ra Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent D., Ra Raichelt J., Kauer G., Liguori R., Vitale D., Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., Edward P., Masuy D., Edward P., Masuy D., Edward P., Mewes H.-W., Ra Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallion L.J., Jenkins J., Ra Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallion L.J., Jenkins J., Ra Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P., Ra Prauss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Ra Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E., Ra Rayokawa C., Kohara M., Matsumoto M., Matsuno A., Murzaki A., Ra Watanabe A., Yamada M., Yasuda M., Tabata S., Rat Watanabe A., Yamada M., Yasuda M., Tabata S., Rat Watanabe A., Yamada M., Yasuda M., Tabata S., Rat Watanabe A., Yamada M., Yasuda M., Tabata S., Rat Watanabe A., Yamada M., Yasuda M., Tabata S., Rat Watanabe A., Watanabe 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=21016720; PubMed=11130713;
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Pfam; PF03468; XS; 1.
Pfam; PF03470; zf-XS; 1.
Hypothetical protein.
SEQUENCE 635 AA; 73841
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Pfam; PF03
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EMBL; AC069474; AAG51004
InterPro; IPR005379; XH.
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                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative transcription factor XI.
Triticum monococcum (Binkorn wheat) (Small spelt).
Triticum monococcum (Binkorn wheat) (Small spelt).
Triaticum transcription wheat)
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooceae; Pooldea:
Triticeae; Triticum.
                                                                                                                         (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIINE=21898330; PubMed=11901130;
Li W., Gill B.S.;
"The colinearity of the Sh2/A1 orthologous region in rice, sorghum "The colinearity of the Sh2/A1 orthologous region in the "The colinearity of the Sh2/A1 orthologous region in the "The colinearity of the Sh2/A1 orthologous region in the "The colinearity of the Sh2/A1 orthologous region in the "The colinearity of the Sh2/A1 orthologous region in rice, sorghum
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InterPro;
InterPro;
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Genetics 160:1153-1162(2002).
                                                                           EMBL; AF434705;
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; IPR005380; XS.
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                          IPR005379;
IPR005380;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03469; XH; 1.
Pfam; PF03468; XS; 1.
Pfam; PF03470; zfz XS; 1.
SEQUENCE 639 AA; 73250 MW; 6A7FD7940030F997 CRC64;
                                                                                         450 KINELSEELQDK 461
                                                                                                                                                                                       334 ELESKMSELNARSKELDDLAAKSSHDKSNLEQEKQKNAIKSNHLKLATAEQQR----ADE-389
                                                                                                                                                                                                                                                                                                                                                                                                                                          394 SGGVRQLYGFLATKQDL---------------DIFNQHSQGKTRLKFELKSYQEM 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 LSQFCPLKVIPLWNFRGHTGNAIVEFAKNWNGFRNALAFEKYFEAGGCGRRDW--KQNWN 215
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                                             606 EFDEALEQLMYK 617
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                                                                                                                                                                                                                                                                                              274 KNKYLQELELRYNETTVSLEKMMGQREQRLQAYNEEIRKMQQLARRHSEKIIDENQNLRS 333
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Search completed: April 6, 2004, 19:34:52 Job time : 49 secs

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Title: Perfect score:

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Scoring table:

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 21, Appl
Sequence 1, Appli
Sequence 72, Appli
Sequence 94, Appl
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Sequence 2, Appli
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Sequence 31, Appli
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Sequence 154, Appli
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Sequence 114, Appli
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Result No.

Score

182 179.5 1173.5 167.5 167.5 166.1 166.1 166.1 164.1 163.1 162.1 163.1 163.1 169.1 159.5 1

Database :

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		Sequence 378, App	Sequence 378, App	Sequence 4, Appli	Sequence 1, Appli	Sequence 4, Appli	4	Sequence 4, Appli	4	Sequence 4, Appli	Sequence 2, Appli	Sequence 6274, Ap	Sequence 15754, A	Sequence 1, Appli	Sequence 24, Appl	Sequence 4, Appli	Sequence 507, App

ALIGNMENTS

B	Dъ	V2	В	γ	망	γQ	Db	Ş	Вb	β	Query Match Best Local Matches 11	; ORGAN US-09-418	; LENGTH: 1	SEO ID NO	, PRIOR	; PRIOR	; PRIOR		PRIOR	CURRENT	; FILE R	; TITLE	GENERAL INFO	Patent	: Seguence	RESULT 1
356 VLMFESSATGYLEAERLHRELAEMGLDRIAMGQKRSMFSGGVRQLYGFLATKQDLDIF 413 : : : : : : : : : : : : : : : : : : :	634 KEEDVIPRIRAMEGRRGRPPNPDRQRAREESRMRRKKGRPPNVGNA 679	304PPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKYEALRARHSYGPQGHRGMS 355	574 VAYYAPCGKKLRQYPEVIKYLSRNGIMDISRDNFSFSAKIRVGDFYEARDGPQEMQWCLL 633	276 GASVIPCGEIYGOW	514 SESQSPAFLGTSSSTLTSSPHSGTSKRRRVTDERELRIPLEYGWQRETRIRNFGGRLQGE 573	240 WYNLHPLLAHARTKGARRVKLHRELAEVLEKDLQMR 275	454 DDDDKDQDESDSDTEGEKTSMKLNKTTSSVKSPSMSLTGHSTPRNLHIAKAPGSAPAALC 513	184DDYDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQINEPQRQWHCPACQNGPGAID 239	394 QFRGTDSDIPSSKDSEDSNEDEEEDDEEDDEEDDESDDSQSESDSNSESDTEGSEEE 453	140 QARGGSAQHTAVQEFPDVEDDVDNASEEENDSDALDDSDDDLAS 183	Match 5.5%; Score 182; DB 4; Length 1972; Local Similarity 20.8%; Pred. No. 1.8e-05; Local Similarity 83; Mismatches 190; Indels 158; Gaps 20	ORGANISM: Homo sapiens 09-418-710-21	LENGTH: 1972 TYPE: PRT	FastSEQ for	FILING DATE: 1997-04-18	ã	FILING DATE: 1997-10-24	1998-04-17	PPLICATION NUME	F PILING DATE: 1999-10-15	FERENCE: 06501-04200	VENTION:	TNE C	0. 6596482	21. Application US/09418710	710-21

Indels

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Gaps

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US-08-685-576-1
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                                                                                                                                                                                                                                FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
ATTORNEY/ACENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FREDEN: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                 REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 7-325129 FILING DATE: 20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                               TOPOLOGY:
                                                                              TYPE: amino acid
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                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 NQHSQGKTRLKFELK-SYQEMVVKELRQISEDN----QQLNYFKNKLSKQNKHAKVLEES
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IVENTION: RHO TARGET
SEQUENCES: 16
                                                                                                  1388 amino acids
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Nakano, Takeshi
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                                                                                                                                                                       (202) 672-5399
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Score 179.5;
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   Length 1388;
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                                                                                                               ; TYPE: PRT
; ORGANISM: HOMO
US-09-418-710-72
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: ,
PRIOR FILLING DATE: 1997-04,
PRIOR FILLING DATE: 1997-04,
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FASCSEQ for Windows
SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-418-710-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 72, Application US/09418710 Patent No. 6596482
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                              Query Match
Best Local Similarity
                                           Matches 128;
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jones, Michael H. TITLE OF INVENTION: TRANSCRI
                                                                                                                                                                      ENGTH:
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            47 ISKKNKNKPGNTSGKTWVSQNSNPPRAWGGQQQGRGSNVSGRGNNVSGRGNGNG-----
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tive 108; Mismatches 182;
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                                                                     5.2%;
                                                                                                                                                                                                            Windows Version
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                                                    Score 173.5; DB 4;
Pred. No. 8.6e-05;
4; Mismatches 213;
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Query Match

DB 4;

Length Indels

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RESULT 4
US-08-056-200-94
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APPLICANT: I
                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                  STREET: 620 Newport CITY: Newport Beach
                     APPLICATION NUMBER: US/08/056,200 FILING DATE: 30-APR-1993
                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                               ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         843
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                                                                                                                                                                                                                                                        CA
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Kim, In-Gyu
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                                                                                                                                                            Floppy disk
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US-08-800-644-94
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 94, Appli
Patent No. 5958752
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Best Local Similarity
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APPLICANT: Steine:
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                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                        APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3
TITLE OF INVENTION: Mehods of Using Same
NUMBER OF SEQUENCES: 117
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TOPOLOGY: linear
MOLECULE TYPE: prot
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TELEPHONE: (714) 760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRAFION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
COMPUTER READABLE FORM:
                                                                                                                                                        CORRESPONDENCE ADDRESS
                   CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
                                                                                                            STREET:
                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F----EMLQQQERAKVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREML 581
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                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08800644
                                                                                                              E: Knobbe, Martens, 620 Newport Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1898 amino acids
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                                                                                                                                                                                                                                                                                               Lee, Seung-Chul
Kim, In-Gyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (714) 760-9502
                                                                                                                                                                                                                                                                                                                                                 Steinert, Peter M.
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Sixteenth
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CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/056,200

FILING DATE: 30-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fedrick, Michael F.

REGISTRATION NUMBER: 36,799

REGISTRATION NUMBER: 31,799

REFERENCE/DOCKET NUMBER: NUMBER: 00

TELECOMMUNICATION: 760-0404
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US-08-728-323A-2
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                     ; Sequence 2, Application
; Patent No. 5948676
; GENERAL INFORMATION:
APPLICANT: Chang, Y
APPLICANT: Bohenzky
APPLICANT: Russo, Y
APPLICANT: Edelman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/800,644
FILING DATE: 14-FEB-1997
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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COMPUTER: II
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)GY: linear
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                                                                                                                                                                                                                                                                                 IKDQEKK--MEDMKKRHHEEIFDLEKEFDEALEQLMYKHG---LHNED 624
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                                                                                                                                            Application US/08728323A
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Chang, Yuan
Bohenzky, Roy A.
Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-728-323A-2
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Best Local Similarity
              APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EDISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-19
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ANAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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Pred. No. 0.00016;
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                                                                                    RESULT 9
US-09-595-684B-31
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SEQ ID NO 2
LENGTH: 1162
TYPE: PRT
Sequence 31, Application US/09595684B Patent No. 6544766 GENERAL INFORMATION:
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APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
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LENGTH: 1162
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5.0%; Score 166; DB 4;
Best Local Similarity 19.6%; Pred. No. 0.00016;
Matches 46; Conservative 66; Mismatches 85
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CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
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Local Similarity 19.6%; Pred. No. 0.00016;
hes 46; Conservative 66; Mismatches 85
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TITLE OF INVENTION: Human kinesins and methods of
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: Cytop036
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
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TYPE: PRT
ORGANISM: Human
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                               NA----LESLKHQETINTLKSKISEEVSRNLHMEENTGETKD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EVILLSELKSLPSEVERLRKEIQDKSEELHIITSEKDKLFSEVVHKESRVQ 792
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                                                                                                                                                                                                                                                                     EAQKFDSSLGALKTELSYKTQELQE----KTREVQERLNEMEQLKEQLENRDSPLQTVER
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VAisberg, Eugeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.0%; Score 164.5; DB 4;
18.2%; Pred. No. 0.00067;
ative 134; Mismatches 271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DIFNQHS
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US-08-685-871-2
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GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICANT: IWAMATSU, AKIHIYO
TITLE OF INVENTION: RHO TARGET PROTEIN KINASE
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-
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PRIOR APPLICATION NUMBER: (APPLICATION NUMBER: (CAPPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/845
REFERENCE/DOCKET NUMBER: 16887/845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 1354 amino aci
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CITY: Washington
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                                                  657 DMLNHSEKE-----KINLEIDLNYKLKSL-QQRLEQEVNEHKVTKARLTDKHQ 703
  350 G-HRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGQKR-SMFSGGVRQLYGFLATK 407
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                                                                                                                                                   AILEAERRDRGHDSEMIGDLQARITSLQEEVKH-LKHNLE-----KVEGERKEAQ 656
                                                                                                                                                                                                   PLL-AHARTKG------ARRVKLHRELAEVLEKDLOMRGASVIPCGEIYGQWKG--
                                                                                                                                                                                                                                                        DILRTESDTAVRLRKSHTEMSKSISQLESIN-RELQERNRILENSKSQTDK---DYYQLQ 607
                                                                                                                                                                                                                                                                                                                                                                                                    OHTAVQEFPDVEDDVDNASEEENDSDALDDSDDDLASDDVDSDVSQKSHGS------
                                                                                                    --LGEDEKDYEIVMPPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKYEALRARHSYGPQ 349
                                                                                                                                                                                                                                                                                                  OHRINEYORKAEQENEKRNVENEVSTIKDOLEDIKKVSONSOLANEKLSOLOKOLEEAN 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202) 672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.0%; Score 164; DB 3; Length 1354;
21.3%; Pred. No. 0.00029;
ative 89; Mismatches 201; Indels 146;
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US-08-685-576-4
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                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 8-131206
APPLICATION NUMBER: JP 896
APPLICATION TOMBER: JP 8-131206
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 166
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 7-
APPLICATION UNMBER: JP 7-
FILING DATE: 20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-NOV-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                          FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                      TELEFAX: \L. 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-JUL-1996
                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 QIHERRDAK-EENFEMLQQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            802 GLEKOMKQEINTLLEAKRILEFELAQLIKOYRGNEGOMRELODQLEAEQYFSTLYKTQVK 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536 KAACOOOONINGSSNDDCKKYVEEARSELIELOEKEWEELAEVEHTIKDOEKKWEDWKKK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862 ELKEETEEKNRENLKKIQELONEKETLATQLDLAETKAESEQLARGLLEEQYFELTQESK 921
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                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi, No. 5906819uaki
VENTION: RHO TARGET PROTEIN RHO-KINASE
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Nakano, Takeshi
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                                                               1388 amino acids
                                                                                                                                                                 (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: JP 8-17150
05-JAN-1996
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Akihiro
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; MOLECULE TYPE:
US-08-685-576-4
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                                               NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 154
LENGTH: 966
                                                                                                                                                                                                                                                                                                                                                          Sequence 154, Application US/09688188B
                                                                                                                                                                                                                                                                                                                        Patent No. 6656716 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 110;
                                                                                                                  APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
FRIOR APPLICATION NUMBER: 09/291,417
PRIOR PILING DATE: 1999-04-14
PRIOR PILING DATE: 1998-04-14
PRIOR PILING DATE: 1998-04-14
 -09-688-188B-154
                                                                                                                                                                                                                                                                                    APPLICANT:
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               ORGANISM: Murine sp
                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KMEDMKKRHHEEIFDLEKE
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Best Local S
Matches 138
                                                                                                                  Sequence 154, Application US/09291417D
PATENT NO. 6680170
GENERRAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WASTINEZ, BAULD
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
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18.3%; Pred. No. 0.00026;
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RESULT 14
US-09-914-259-11
US-09-914-259;
Sequence 11, Application US/09914259;
Sequence 11, Application US/09914259;
Patent NO. 6495336;
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Myman, Paul
APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF
FILE REFERENCE: 8471-010-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Murine sp.
US-09-291-417D-154
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDSANVTQPSLDSNK--LLQDSSTPLPPSQPQE----PVNGPCSQPSGDG-----PLQTT 390
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18.3%; Pred. No. 0.00026;
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                    OF NANOSTRUCTURES
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; TYPE: PRT
; ORGANISM: HOMO
US-09-914-259-11
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CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 3878
                                                                                                                                                                                                                                                                                             RESULT 15
US-08-938-105-3
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Best Local Similarity
                                                                                                                                                                              Sequence 3, Application US/08938105
Patent No. 6353151
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Viketrom, Karen L.
APPLICANT: Viketrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL
                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: Sheridan Ross P.C.
ADDRESSEE: Sheridan Ross P.C.
ADDRESSEE: January Lincoln St., Suite
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                       STATE:
                                                                                             CITY: Denver
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ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3595-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1886 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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1719 KKEQDTSAHLERMKKNMEQTIKDLQHRLDEA-EQIALKGG 1757
                                                                                                      1659 SERVQLLHSQNTSLINQKKKMDADLSQLQTEVEEAVQECRNAEEKAKKAITDAAMMAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                             1494 EEAEASLEHEEGKILRAQLEFNQIKAEIERKLAEKDEEMEQ-----AKRN-HLRVVD 1544
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                                                 582 IKDQEKK--MEDMKKRHHEBIFDLEKEFDEALEQLMYKHG 619
                                                                                                                                                           505 DRFFM------DSIKQ---IHERRDA-----KEENFEMLQQQERAKVVGQQQ---- 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 AHARTKGARRVKLHRELAEV--LEKDLQMRGASVIPCGEIYGQWKGLGEDEKDYEIVWPP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 GSRKQNK------WFKKFFGSLDSLS-IEQINEPQRQWHCPACQNGPGAIDWYNLHPLL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 WQARGGSAQHTAVQEFPDVEDDVDNASEEEND-SDALDDS--DDDLASDDYDSDVSQKSH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDLDIFNQHSQGK-TRLKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAKV-- 464
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Search completed: April 6, 2004, 19:36:00 Job time : 26 secs

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Perfect score:
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Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1428.5 745.5 721 721 297 258 199.5 199.5 199.5 178.2 178.2 173.5 172.5	Score
44 44 44 44 44 44 44 44 44 44 44 44 44	Query Match Length
324 223 188 219 2219 227 414 418 1972 1203 1879 1969 1969 1969	
12 12 12 12 12 13 14 14 14	DB
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Sequence 58390, A Sequence 234018, Sequence 234019, Sequence 242612, Sequence 178379, Sequence 68998, A Sequence 63998, A Sequence 54044, A Sequence 21, Appl Sequence 1265, App Sequence 71, Appl Sequence 71, Appl Sequence 295, App Sequence 43, Appl Sequence 33, Appl Sequence 102, Appl Sequence 102, Appl	Description

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4.9	4.9	4.4	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1
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00	Sequence 47, Appl			Sequence 2, Appli				6527		15,	3304	3191		1586		Sequence 2, Appli				Sequence 4, Appli	æ	е4,	Sequence 79, Appl	78,	14,	,	-

ALIGNMENTS

Qy 127 -PVSRPPLEGGWNWQARGGSAQHTAVQEFPDVED-DVDNASEEENDSDALDDS	Qy 74 WGGQQQGRGSNVSGRGNNVSGRGNGNGRGIQANISGRGRALSRKYDNNFVAPP	Qy 33 RLASSQDDGGEWEVISKKNKNKPGNTSGKTWVSQNSNPPRA	Query Match 43.1%; Score 1428.5; DB 12; Length 61 Best Local Similarity 47.2%; Pred. No. 2.4e-99; Matches 294; Conservative 99; Mismatches 159; Indels 71	Publication No. US20040034888A1 GENERAL INFORMATION: APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement ITILE OF INVENTION: NUMBER: US/10/425,114 CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT APPLICATION SEGUID-04-28 NUMBER OF SEG ID NOS: 73128 SEQ ID NO 58390 LENGTH: 611 TYPE: PRT ORGANISM: Zea mays FEATURE: OTHER INFORMATION: Clone ID: LIB3079-030-A8_FLI.pep US-10-425-114-58390	; sequence 58390, Application 05/10425114
OVDNASEEENDSDALDDS 177	ALSRKYDNNFVAPP 126 	7VSQNSNPPRA 73 	Length 611; ndels 71; Gaps 15;	Molecules Associated With t Improvement /	

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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecul
TITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234018
LENGTH: 324
                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
FERTURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_53342C.1.pep
US-10-424-599-234018
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Publication No. US20040031072A1
                                                                                                                                                                                        Matches 162;
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Best Local Similarity
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                                                SEEENDSDALDDSDDLASDDYDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQINEPQR
                                                                                                                                       GRGRALSRKYDNNFVAPPPVSRPPLEGGWNWQARGGSAQHTAVQEF--PDVEDD--VDNA 164
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QWHCPACQNGPGAIDWY-NLHPLLAHARTKGARRVKLHRELAEVLEKDLQMRGASVIPCG
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                                                                                                                      GRPQLGTSGYESNYVTPNPVIRPPLEHGWNWQSRPGAIQSNVRDEISPEDLQKNYGVDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREMLIKDQEKKMEDMKKR
                                                                                                                                                                                        Conservative
                                                                                                                                                                                    22.5%; Score 745.5; DB 1
31.1%; Pred. No. 4.3e-48;
tive 68; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecules and Other Molecules Associated Thereof for Plant Improvement
                                                                                                                                                                                                                    DB 12;
                                                                                                                                                                                    84; Indels 207;
                                                                                                                                                                                                                     Length
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APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecu:
TITLE OF INVENTION: Plants and Uses Thereo:
FILE REFERENCE: 38-21(5322))B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEO ID NOS: 285684
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Best Local Simil
Matches 131; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 234019
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                      FEATURE: unsure
LOCATION: (1)..(223)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine
                                                                                                                                                                                                                                                                                       Local Similarity
   180
                                  284
                                                                   120
                                                                                                    225
                                                                                                                                                     165 SEEENDSDALDDSDDDLASDDYDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQINEPQR 224
                                                                                                                                                                                                                                       109
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                                                                                                                                     13
                                                                                        QWHCPACQNGPGAIDWY-NLHPLLAHARTKGARRVKLHRELAEVLEKDLQMRGASVIPCG
                                                                                                                                                                                                      GRPQLGTSGYESNYVTPNPVIRPPLEHGWNWQSRPGAIQSNVRDEISPEDLQKNYGVDDD
                                                                                                                                                                                                                                     GRGRALSRKYDNNFVAPPPVSRPPLEGGWNWQARGGSAQHTAVQEF--PDVEDD--VDNA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQEKKMEDMKKRHHEEIFDLEKEFDEALEQLMYKHGLHNED 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLEESLEIMSEKLRRTAEDNRIVRQRTKMQHEQNREEMDAHDRFFMDSIKQIHERRDAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSYGPQGHRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGQKRSMFSGGVRQLYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIYGQWXGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDXWLGMGNQELLEYFDKYEALRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QWHCPACQGGPGAIDWYRGLQPLVTHAKTKGSKRVKIHRELAILLDEELRRRGSAVIPPA 179
   EVFGKWKGLKEEEXDHEIVWPPMVVIQNTKLEQDENDK
                   EIYGQWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDK
                                                                  QWHCPACQGGPGAIDWYRGLQPLVTHAKTKGSKRVKIHRELAILLDEELRKRGTSVIPAG
                                                                                                                                     GEER-ESDDLEDTDDDLMSDDDDSDASQKSHETRKKSKWYKKFFEILDGLTVEQINEPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHKDNVDAMTRRHWEEKVQLEERFNEELAKLMEKYSLSHPE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENFEMLOQQERAKVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREMLIK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LATKQDLDIFNQHSQGKTRLKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEFERMQQEKREKV----KPSSTSPLNEEEGRVKVDEYLKFVEFQDKEMENFVAEEEKLRQ
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         max
                                                                                                                                                                                                                                                                                      21.8%;
                                                                                                                                                                                                                                                                    ; Score 721; DB 12;
; Pred. No. 1.9e-46;
41; Mismatches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecules and Other Molecules
Thereof for Plant Improvement
                                                                                                                                                                                                                                                                        40;
                                  321
                                                                                                                                                                                                                                                                                                       Length 223;
                                                                                                                                                                                                                                                                        Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_132093C.1.pep
US-10-424-599-178379
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, Sequence 178379, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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US-10-424-599-242612
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                                                                                                                                                                             APPLICANT: Cao Yongwei
TITLE OF INVENTION: Sy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 178379
LENGTH: 219
TENER.
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 242612
LENGTH: 188
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                     Query Match
Best Local Similarity
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                                                                                                                            FEATURE:
                                                                                                                                             ORGANISM: Glycine max
                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT3847_61108C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 9.0%;
Local Similarity 33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 LKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAKVLEESLEIMSEKLRRTAEDNRIV 486
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Zhou Yihua
    Conservative
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                   7.8%; Score 258; DB 12; 33.6%; Pred. No. 1.8e-11;
  24;
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    Mismatches
                                        DB 12; Length 219;
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    Indels
    40;
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Gaps
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; OTHER INFORMATION:
US-10-425-114-68998
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US-10-425-114-68998
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                                                                                                                  Sequence 63998, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
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Publication No. US20040034888A1
GENERAL INFORMATION:
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LENGTH: 227
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Best Local Similarity
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)18
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                                                                                                                                                  389 KRSMFSG----
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                                                                                                                                                                                                                                                                                                                                                                                                                             337 ----YEALRARHSYGPQGHRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGQ--- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 CPACQNGPGAIDWYNLHPLLAHARTKG----ARRVKLHRELAEVLEKDL-----QMRGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GRALSRKYDNNFVAPPPVSRPPLEGGWNWQARGGSAQHTAV------QEFPDVEDD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 SVIPCGEIYGQWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDK- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                 MTELGFSGGKSKSLYGKEGHMGLTLIKFANNSSGLKEAERLAEYLERQDRGRIGWSRAHA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSLP----SDLVQASREDLIVWPPTVIIHNTSTGRKKDGRLEGLGNKEM----DKK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLAC--GRSSKDFADVHGLVMHAYNPPNADSLVDHLGLHKALCVLMGWDYTKVPENFKGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDNASEEENDSDALDDSDDDLASDDYDSDVSQKSHGSRKQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LTASESESSNIVTSNPVIRPPLEHGWNWQSISGSKQSKSVDDSLVKGEISEESPMKQPF 176
                                                                                                                                                                                                                                                                                      SRSVDSDQNPLLVETDTRTAEKKRILYGYLAIASDLDELDSDSRKRASLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone ID: UC-ZMROTEOSINTE006D03_FLI.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 199.5; DB 27.0%; Pred. No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                -GVRQLYGFLATKQDLDIFNQHSQGKTRLK 424
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53313)B
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 63998
LENGTH: 414
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US-10-425-114-54044
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                                                                                                                                                                                                                                                                                                                                  Sequence 54044, Application US/10425114 Publication No. US20040034888A1
                                                  APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54044
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                           APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
ORGANISM: Zea mays
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                                      ENGTH: 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRELAEMGLDRIAWGQKRSMFSGGVRQLYGFLATKQDLD----IFNQHSQGKTRLKFELKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAKVLEESLEIMSEKLRRTAEDNRIVROR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESHFAAGGFGKKDWIGKKNOGS----ELYGWLARAEDYNSPGIIADH----LRKNGDLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEKAVHRALFKYLKNGLAKSPEPGSHATPV-----EPQPLQNRDEKFVWPWMGVLVNV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KIYARLMSGDL-KLNKNGENYICPFCSSKKKN---YSKSSLVQHASGVSAAPNREA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           --NDLDVRSKQLDEIAAKSDYDRRSLEQ--EKQKNAIKSSHLKLATLEQQKADE 406
                                                                                                                                                                                                 Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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; OTHER INFORMATIONS-10-425-114-54044
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PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: PT 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: UP 9/116570
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-39-479-21
US-09-39-479-21
Sequence 21, Application US/09839479
Publication No. US20020039779A1
GENERAL INFORMATION:
GENERAL INFORMATION: TRANSCRIPTIONAL
TITLE OF INVENTION: TRANSCRIPTIONAL
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Best Local 9
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CURRENT FILING DATE: 2001-04-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1972
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les 62; Conser
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les 113; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 CLAC--GRSSKDFADVHGLVMHAYNPPNADSLVDHLGLHKALCVLMGWDYTKVPENFKGY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 CPACQNGPGAIDWYNLHPLLAHARTKG-----ARRVKLHRELAEVLEKDL-----QMRGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 QSLP-----SDLVQASREDLIVWPPTVIIHNTSTGRKKDGRLEGLGNKEM----DKK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 SVIPCGEIYGQWKGLGEDEKDYEIYWPPMVIIMNTRLDKDDNDKWLGMGNQELLEYPDK- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 KRSMFSG------GVRQLYGFLATKQDLDIFNQHSQGKTRLK 424
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                                                                                                                                                                                                     240 WYNLHPLL-----AHARTKGARRVKLHRELAEVLEKD-----
                                                                                                                                                                                                                                                                             184 -- DDYDSDVSQKSHGSRKONKWFKKFFGSL--DSLSIEQINEPQRQWHCPACQNGPGAID 239
                                              304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRSVDSDQNPLLVETDTRTAEKKRILYGYLAIASDLDELDSDSRKRASLQ 439
                                                                                                                                                                                                                                                                                                                         OFRGTDSDIPSSKDSEDSNEDEEEDDEEEDDEDDESDDSQSESDSNSESDTEGSEEB 453
                                                                                                                                                                                                                                             DDDDKDQDESDSDTEGEKTSMKLNKTTSSVKSPSMSLTGHSTPRNLHIAKÅPGSAPAÅLC 513
                                                                                  VAYYAPCGKKLRQYPEVIKYLSRNGIMDISRDNFSFSAKIRVGDFYEARDGPQEMQWCLL
                                                                                                                                                               SESQSPAFLGTSSSTLTSSPHSGTSKRRRVTDERELRIPLEYGWQRETRIRNFGGRLQGE
                       -----PPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKY---EALRARHSYGPQGHRGMS 355
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                                                                                                                                                                                                                                                                                                                                                                                                        5.5%; Score 182; DB 12; illarity 20.8%; Pred. No. 0.00018; Conservative 83; Mismatches 190;
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Length 1972; Indels 158;

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RESULT 10
US-10-097-340-43
// Sequence 43, Application US/10097340
// Publication No. US20030087250A1
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                                                         US-10-097-340-43
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR PELICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR PELICATION NUMBER: 60/276,026
PRIOR PELICATION NUMBER: 60/276,026
PRIOR PELICATION NUMBER: 60/324,967
PRIOR PELICATION NUMBER: 60/324,967
PRIOR PELICATION NUMBER: 60/311,732
PRIOR PELICATION NUMBER: 60/311,732
PRIOR PELICATION NUMBER: 60/311,732
PRIOR PELICATION NUMBER: 60/325,102
                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 43
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030 CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT FILING DATE: 2002-03-14
                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19
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                                                                       ORGANISM: Homo sapiens
                                                                                                               ENGTH:
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Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
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Sebastian HOERSCH
Shubhangi KAMATKAR
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Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordon B. MILLS
Robert C. BAST,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peter VEIBY
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5.4%;
19.0%;
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Score 178; DB 14;
Pred. No. 0.00019;
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                   Length 1203;
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           US-10-296-115-1265
; Sequence 1265, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
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                                                                                          RESULT 11
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APPLICANT: Hyseq Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 PLLAHARTKGARRVKLHRELAEVLEKDLOMRGASVIPCGE---IYGQ------WKG 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VSQNSNPPRAWGGQQQGRGSNVSGRGNNVSGRGNGRGI----QANISGRGRALSRKYD 119
                                                                                                                                                TSGGLSRLQD
                                                                                                                                                                                                                                                                                                                                  LQQQE----
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                                                                                                                                                                                     YKHGLHNEDD
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                                                                                                                                                                                                                                                          ----KEMEEFVEEREMLIKDQEKKMEDMKKRHHEEIFDLEKEF-DEALEQLM 615
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FILE OF INVENTION: No. US20040053248Alel NU
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1265
LENGTH: 1879
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: MANE/KEY: misc_feature
LOCATION: (1)...(1879)
OTHER INFORMATION: Xaa = any amino acid or
US-10-296-115-1265
             Sequence 71, Application US/09839479
Publication No. US20020039779A1
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
APPLICANT: JONES, MICHAEL H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1355 LLAEEKNIŚSKYADĖRDR-----
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cal Similarity 20.2%;
116; Conservation
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                                                                                                                                                                                                  VKOLKROLEEAEEESQRINANRKKLQRELDEATE 1819
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Pred. No. 0.00057;
14; Mismatches 194;
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; ORGANISM: Homo sapiens
US-09-839-479-71
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                        US-10-363-616-295

| Sequence 295, Application US/10363616

| Publication No. US20040044181A1

| GENERAL INFORMATION:

| APPLICANT: Hyseq, Inc

| TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
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PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
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Best Local Similarity
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PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGNQELLEYFDKY---EALRARHSYGPQGHRGMSVLMFESSA--TGYLEAERLHRELAEM 379
                                                                                                                                                                                                                                                                                                                                QQIRMEKELRAQQILEAKKKKKEEAANAKLLEAEKRİKEREMR------RQQAVLLK
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; Pred. No. 0.00079;
94; Mismatches 213;
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                                    POLYPEPTIDES
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Matches Query Match

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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN

ITITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

DETION ADDITIONATION NUMBER: US/10/369,493
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; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 295
; LENGTH: 593
; TYPE: PRT
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US-10-363-616-295
                                                                                                                                                                                                                                                                                      Sequence 43, Application US/10369493 Publication No. US20030233675A1
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PRIOR APPLICATION NUMBER: US 60/360,039
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                                                                                                                                                                                                                                                                                                                                                                                                                                  550 QDVYVELSHIKTRSEREIEQLKEHLRLAMAALQEKESMRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 YLEAERLHRELAEMG-----LDRIAWGQKRSMFSGGVRQLYGFLATKQDLDIFNQHSQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVPAGE--GPRRGLG------APLTEDQQNRLSEEIEKKWQELEKLPLRENKRVPL
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US-10-205-219-102

Sequence 102, Application US/10205219

Publication No. US20030138803A1

GENERAL INFORMATION:

APPLICANT: Warner-Lambert Company

APPLICANT: Lee, Kevin

APPLICANT: Dixon, Alistair
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 43
LENGTH: 1156
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SEQ ID NO 102
LENGTH: 892
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Best Local Similarity
Matches 82; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use
FILE REFERENCE: WL-A-018200
CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
                                                                                                                                                                     TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
654
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SUMMARIES

REFERENCE AUTHORS TITLE Result No. RESULT 1 AX078760 LOCUS DEFINITION ACCESSION VERSION SOURCE ORGANISM KEYWORDS 00000 იი იი იი იი 000000 Score AX078760 Sequence 1 f AX078760 AX078760.1 Arabidopsis thaliana (thale cress) Arabidopsis thaliana Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Beclin, C., Elmayan, T. and Vaucheret, H Novel sgs3 plant gene and use thereof Match .7 80318 7 110000 7 133120 7 154923 7 154923 7 154923 7 174641 7 177529 7 177529 7 177529 7 177834 7 17934 7 17934 7 179334 7 179328 7 17934 7 17937 7 193936 7 193936 7 193936 7 193936 7 193936 7 193936 .4 45 .7 170765 101080 101241 1012716 126716 152345 180925 Length 3275 bp from Patent W00105951. GI:13158379 650 멂 AC048381 D84313 AX349428 AX344692 AX346143 AL645798 AC107170 HS393P23 AC006044 AC145578 AC007429 AC007429 AC018811 AC0121725 AC012887 AC012271 AC012887 AC012277 AC012887 AC012277 AC012277 ATCHRIV47 AC107451 AC113572 AC1137942 AC128938 AC107462 BX001014 AL928719 AF057056 BX004860 AL845510 AC107028 BX005128 ATH527741 AC102284 AF239719 BT002944 AX078761 BT004380 ATH528171 AX078760 AB025633 Ħ ALIGNMENTS DNA linear AB025633 Arabidops AF39719 Arabidops BFT002944 Arabidops BX078761 Sequence BT004380 Arabidops AX078761 Sequence BT004380 Arabidops AX528171 Arabidops AX528171 Arabidops AX528171 Arabidops AC107284 Mus muscu AF057056 Uroleucon EX004860 Danio rer AL845510 Zebrafish AC107028 Homo sapi BX005128 Zebrafish AC048381 Homo sapi BX044831 Drosophila AX348428 Sequence AX346439 Sequence AX346439 Sequence AX3464692 Sequence AX346148 Sequence AX346149 Homo sapi AC0119271 Mus muscu AC0119871 Homo sapi AC0119727 Rattus no AX0119607 Rattus no AX0119607 Rattus mo AX119607 AL161547 AC107451 AC113572 Description AC137942 PAT Sequence Arabidops 22-FEB-2001 Mus muscu Mus muscu

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                                                 source
                                                                                   Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MQM1
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
MetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
splicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/ggi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazus.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
Tel:81-438-52-3935, Fax:81-438-52-3934)
On Sep 15, 2000 this sequence version replaced gi:4589439.
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20181125
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Structural analysis of Arabidopsis thaliana chromosome 5.
Sequence features of the regions of 3,076,755 bp covered
Pl and TAC clones
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/strain="Columbia" /db_xref="taxon:37

_xref="taxon:3702"

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/translation="MAYOPGTSVDESPAHKKVDETPPKHVQFLEPISKTVVDDAQNPS
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QPLDDRNRKGKRFAFGKYRYDLTVLLDVHTLLFSADCFSVFFFFMWFAIFICYFLISGG
QPLDDRNGSNLEKTLAFGHASYKVSLAVGFVDIWEAATLSIKREGYSIKCISDLTIAE
KFSASTTVTIPFGQPAELVIIGSDGSEHSLRADNGSPDLIGSRDEIVLTLRLFIKRVM
FFKALNSFYHFRCSCHKSRGNL"
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join(3184. .3403,3474. .3595,3681. .3723,3777. .3898,
4042. .4198,4445. .4515,4601. .4714,4888. .4988,5300.
/note="gb|AAF01580.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MODGTSVYESPALMOADETPPISKTVVNDTKNIFYFDDGDDAPL PALENLOISGEPYFGHELQACGYSINGTTSCHYEMVCHLEDGSVNYIDGAKKENYLYT ADDVGLCLAIEVQPLDDRNRKGELVKVFANDNRKIACHFEMQSNIDKTHTGHASKYV SLAIGFYHIMBAATLSIEREGYYITKCNNDLTITEKFSASTAVKIPFEKPAELVIIGSD GSEHCLRVDNEWPDIRLCKEEKRVLKLVKYVVFEQKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSWMXGKSSGWTAFDLKQRQKQGLESEVEGDPFPPVSTSVNASF
GVRGRLRRNHEPSEKSFSSVLLPPSRRPALTENKDCGNQERGGCCRRKEDTLGLFVNS
HDLAFTYLKEMNSWADDNLIRDVLLSTEDDFRALAFLKGMVSSGKEDEFDTSKIEGY
SSDNRRSEYRTFEKTTYSSVKMARSTFEDAGKYDLENSDGSSFLVNASDNEKFDDI
SELDSIIQRLQSIPIERDWLEDDLYLSHRKDALKVMRSASNHSRAAQNAFQRYDHASA
KQHSDKAREDWLAAEKLNAEAAKKIIGITNKDNDIWKLDLHGLHATEAVQALQERLQM
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7121. .7169,7396. .7466,7550. .7663,7785. .7882,8112. .8181)
/note="gb|AAFF1580.1
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/protein_id="BAA97251.1"
/db_xref="GI:8809710"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (8642. .8705, 8794. .8863, 8978. .9387,
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IGKHSRGQASLPLAVKTFFEDNRYRFDETRPGVITVRPKFRHS"
complement (12417. ..13424)
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/db_xref="GI:8809709"
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similar to unknown protein"
                                                                                                                                                                                                                                                                 / TABBIAL TONE "WANTDSOPNOKLTLELKTRIALTVISTMTDNAQRPDGTINRRFLR
LFDFRAPPNPKPVNIVSTSDFVVDQSRDLWFRLYTPHVSGDKIPVVVFFHGGGFAFLS
LFDFRAPPNPKPVNIVSTSDFVVDQSRDLWFRLYTPHVSGDKIPVVVFHGGGFAFLS
PNAPFYDNVCRRFARKLPAYVISVNYALAPEHRYPAQVDDGFDALKYIENHGSILPA
NADLSRCFFAGDSAGGNIAHNVAIRICREPRSSFTAVKLIGLISIQPFFGGEERTEAE
KQLVGAPLVSEDRTDWGWKAMGLNRDHEAVNVGGPNAVDISGLDYPETMVVVAGFDPL
KDWQRSYYEWLKLCGKKATLIEYPNWFHAFYIFPELFEAGQLIMRIKDFVDERVASLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains similarity to unknown protein gb|AAF27018.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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unknown protein"
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                                                                                                                                                                                                              join(14922.
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                                                                                                                                                  id:MQM1.20"
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THAVATYFFSIRTKSLTYYSESTLQNNGSLYAHIFFARSGPF1DFTDPEYQPLNSFSR
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strong similarity to unknown protein"
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join(16823. .16952,17143. .17320,17412. .17493,17675. .17851,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAGVPMEVNGLMLGEFVDEYTVRVVDVFAMPOSGTGVSVEAVDHVFQTIMMLDMLKQTG
RPEMVVGMYHSHPGFGCWLSGVDINTOQSFEALNQRAVAVVVDPIQSVKGKVVIDAFR
SINPQTIMLGQEPRQTTSNLGHLNKPSIQALIHGLNHYYSIAINYRKNELEEKMLLN
                                                                                                                                                                                 DKYEALRARHS GEOGHRGMSVIMFESSATGY LEAERLHRELAEMGLDRIA MGOKRSM FEGGYRQLYGELATKODIDI FROHSOGKTRLKFELKS Y CEMVYKELROL SEDNQOLNY FRONKLSKOUKHAKVILESILE IMSEKLRRTAEDNRI I VRORTKMOHEONNEEMDAHDRF MDSI KOIHERRDAKERFEMILOQUERAKVVGQOQONINPSSNDDCRKRAEEVSSFIEF OEKMEEFVEEREMLIKDQEKKMEDMKKRHHEBI FDLEKEFDEALEQLMYKHGLHNED
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VDNASEEENDSDALDDSDDLASDDVSDVSGVSHGSRKQNKWFKKFFGSLDSLSIEQ
VDNASEEENDSDALDDSDDLASDDVSDVSGVSHGSRKQKKFKFGSLDSLSIEQ
INEPQRQWHCPACQNGPGAIDWYNLHPLLAHARTKGARRVKLHRELAEVLEKDLQMRG
ASVIPCGEIYGQWKGLGEDEKDYEIYWPPMVIIMNTELDKDDNDKWLGMGNGELLEY
ASVIPCGEIYGQWKGLGEDEKDYEIYWPPMVIIMNTELDKDDNDKWLGMGNGELLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="wdkwnoaiekwkwlvgwevedeqoaadeesslsfwedlwrncal
TTKORFYGFAICLSAGLTCTLLSMLVFFNPVKFGITFTLGNLWALGSTAFLIGPORQV
TWMLDPARIYATALYLASIIIALFCALYVRNKLLTLLAIILEFTGLIWYSLSYIPFAR
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qdakkhleehvsnimssnivqilgimldtvvf"
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/protein id="BAA97246.1"

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28385. .28604,28688. .28855,28944. .29092)
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961 GAAACAATGTATCCGGGAGAGGTAACGGCAATGGTCGGGGCATTCAAGCTAACATATCTG 1020	901 ATCCTCCTAGAGCTTGGGGTGGTCAGCAGCAAGGGAGAGGTAGCAACGTATCTGGGAGAG 960 	841 AGAAGAACAAGAACAAACCAGGAAACACTTCTGGAAAAACTTTGGGTTTTCTCAGAATTCGA 900	781 TGGCAGGACGAGACTGGCTTCTTCACAAGATGATGGAGGAGAGAGTGGGAGGTCATTTCCA 840	721 CTAAGGAAAAGAACGTTCAGGGTGGTTATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTT 780	661 ACTGTGGGTTTCTTTGGTGGCTATAGGTTGTAAAAATGAGTTCTAGGGCTGGTCCAATGT 720	601 ATGCGTTGTTGGCTTGTTATAACTTCACGTTCATGTGTGGATTTTGAGATTTTGGTAGTG 660 .	541 TIGITITCATATAAATCGGATTGATCTACCTTTTGTGCTTTGATGTTTTTTTT	481 TICACCGITTAGICGCIGATCGGAGIAITITGACIGTGAAAAAICCITCGIITITITGGIIT 540	421 TITIATAGITCTTAGGITAACGATACCTGCGTCTTACTGTTTTTGTTCATTTTTGTTGTGCT 480	361 ATTGCCCTAATGTTCTCGATTTCGAACGTTTTTGTGCTATGGGTTACTTTTTTCCCTATA 420	301 CCTCCGATCGCCTCACCGCATGCATTCTGTGCTCGATTTCTCTTTTCTTCGCTGGAAAA 360	241 TCTCCGGCGCTTTAAACTTACGTTCTCCGTCGTTACTCTGTAAGTTTTCTGCCTTAGAG 300	181 ATTTGTCTCTTCGTCAGTTTATTTTCTTCCTCCGGAGTCCTGACTCACTACTCTCAC 240	121 GAAAATTTGGAGTCCAGAATCGGAAAAACGAGGCCGTTTTAGAGCTTAATAAGCTTCCTC 180 	61 TTAAGTTAAGCGAAAAAGGAAAAAAAAAAAAAAAATGAAAATGAAAACAAAATGAAACTGAAT 120 	1 GACAAACAAACAAAATTAAGCAAGTCATGTTCGTAGCAATTAATT	Query Match 100.0%; Score 3275; DB 8; Length 81365; Best Local Similarity 100.0%; Pred. No. 0; Matches 3275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CDS complement(join(2943929576,2966129885,2998530268, 3034130493,3057930722,3095631484)) /note="gene_id:MQM1.15
Qy	g &	94 65	B &	\$ & &	S & &	, B &	o do q	P &	B 5	? B &	S & &	}	B &	B &	}	}	S B &	? B
2041 AATTTGATATATGCTTTTAGTTTTTGTAATTTTAAAGTTTTTGTTGGTCCGTGTTAA 2100	1981 GCAACGAAGCAAGATCTGGACATATTCAATCAACACTCTCAAGGTTCTCTCCCCCCAAAGA 2040 	1921 GCCTGGGGTCAGAAGCGCAGTATGTTTTCTGGAGGTGTTCGCCAACTGTATGGCTTCCTT 1980	1861 GETTATTTGSAGGCCGAACGCCTCCACCGGAGGTTAGCTGAGATGGGGTTAGATAGA	1801 TCCTATGGTCCACAGGGCCATCGTGGATGTTCTGATGTTTGAGAGCAGTGCCACT	1741 ATGGGCAACCAAGAGCTGCTGGAATACTTCCACAAGTATGAGGCTCTTAGAGGACGCCAT 1800	1681 FICHTHAATHTICICTIGCATTCTACTGATCTTAGAATGTTACATTGTAGTGGCTCGGC 23657 TTCTTTAATTTTTCTCTTGCATTCTACTGATCTTAGAATGTTACATTGTAGTGGCTCGGC		1561 GJAAGGSTTTIGGSTIGAGAATIGAAAATAATTIGTICTIGGCCTCCAATIGGTCATCA 1620	1901 AMANGANICIACAGA IGAGAGGCGCA CIGICALICULI IN LIGITAGAGALI IA IGAGGCAGI 2000 1900	1411 ATSCIGAGGACAAAAGGAGCTAGGCGAGTTAAGCTCCATAGAGAAATTGGCTGAAGTTTTAG			261		1191 CAGCING GCAGGAGIII ICCINGANGANIGANG GINGAINAING LI CIGAGGAGAGA CAING CHEANNA 1200 CHEANNA LEAGAGA CHEANNA LEAGAGA CHEANNA LEAGAGAGA CHEANNA LEAGAGAGAGA CHEANNA LEAGAGAGAGAGAGAGAGAGAGAGAAGAGAGAGAGAGAGA	23057 CTCGCCCTCTTTGGAAGGAGGATGGAATTGGCCAGGAGGAGGAGGATCTGCTCAGCACA 2311	1021 GTCGGGGACGACGTTGAGCAGAAGGAATGGAAGGAAGGAA	

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Best Local Similarity
Matches 2254; Conserv
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815 60 755

ATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAAGAACGTTCAGGGTGGTTATAGGCCT

Conservative

68.8%; 5--100.0%; Pr

Score 2254; Pred. No. 0;

BB 8 <u>.</u>

Length 2254;

Indels

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Mismatches

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Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 254)

Mourrain, P., Beelin, C., Elmayan, T., Feuerbach, F., Godon, C.,

Mourrain, P., Beelin, C., Lacombe, A.M., Nikic, S., Picault, N.,

Memoue, K., Sanial, M., Vo, T.A. and Vaucheret, H.

Arabidopsis SGS2 and SGS3 genes are required for

posttranscriptional gene silencing and natural virus resistance

Cell 101 (5), 533-542 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
AF239719
AF239719.1 GI:816402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-FEB-2000) Biologie Cellulaire, Saint-Cyr, Versailles 78026, France Location/Qualifiers
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Beclin, C., Mourrain, P.,
Direct Submission
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/codon_start=1
/product="SGS3"
                                                                                                                                                                                                                                                                                                                    join(<1. .963,1037. .1328,1440.
/product="SGS3"
                                                                                                                                                                                                                                                                                                 join(1. .963,1037. .1328,1440. .1684,1787. .1953,2044.
                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:3702"
chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                             mol_type="genomic DNA"
cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis thaliana"
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61 BAGGITGAACAGTTGCTCAAGAGTTGCCAGGAACACAGAGCTTGCTCCTCCTCACAGATGAT 120 816 GAGGACACAGTTGCTCAAGAGTTGCCACAACACAGACCTTGCTCACAAGATGAT 120 817 GAAGACAGTTGCTCCACAAGATTGCCACAACAACACACTTCCCACAAGACCACTTCCCAAGACCACTTCCCAAGACCACTTCCCAAGACCACTTCCCAAGACCACTTCCCAAGACCAAGACCACTTCCCAAGACCAAGACCACTTCCCAAGACCAAGACCACTTCCCAAGACCAAGACCACTTCCCAAGACCAACCA
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1141 TCTSANGTTIGAGAGCAGTGCCACTGGCTATTTIGAGAGCCGAAGCCCTCCACCGGAGTT 1200 1201 CCTCCACAGGAGCTAGCCTCACCGAGACTT 1201 1202 CTCTCACCTGAATTGCCTGCCCCACAGACCACCACCACCACCACCACCACCACCACCA

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TITLE
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AUTHORS
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AUTHORS
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VERSION
KEYWORDS
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2 (bases 1 to 2162)
2 (wanda,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M. Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satcou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2162 bp mRNA linear Arabidopsis thaliana clone RAFL14-93-K05 (R20243) (At5g23570) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-JAN-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                           submitted to Genbank.
                                                                                                                                                                                                                                                                                                                                                                                          Annotation based on July 2002 version of the Arabidopsis genome
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                                                 /gene="At5g23570"
92. .1969
/gene="At5g23570"
/codon_start=1
                                                                                                         /gene="At5g23570"
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/note="This clone i
                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
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                                                                                                                                                      (lambda PS) as a BamHI/XhoI insert
                                                                                                                                                                                                                       clone="RAFL14-93-K05 (R20243)"
                                                                                                                                                                                                                                             chromosome="5"
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misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTTCA
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                                                                                                                  GATGACGACCTTGCAAGTGATGATTATGACTCGGATGTGAGTCAAAAGAGCCCATGGATCA 1286
                                                                                                                                                                                                                                                                   GAGGATGATGTGGATAATGCTTCTGAGGAAGAGAATGATTCCGATGCTTTGGATGATTCT
                                                                                                                                                                                                                                                                                                      GAGGATGATGTGGATAATGCTTCTGAGGAAGAGAATGATTCCGATGCTTTGGÅTGATTCT
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                      CAGATAAATGAACCACAGAGGCAGTGGCATTGTCCAGCTTGTCAGAACGGACCTGGTGCC
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                                                                       Conservative
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2146
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DKYEALRAHISYGPOGHRGWSVLMFESSATGYLEAERLHRELAEMGLDRI AWGOKRSM
PSGGVRQLYGFLATKQDLDIFNOHSOGKTRLKFELKSYGEMVVEELROIEEDNQOLW
FKYKLSKQNKHAKYLESELEIWSEKLERTAEDNRIVRQRTKWQHEQNREEMDAHDRFF
MDSIKQIHERRDAKEENFEMLOQGERAKYVGGQQQNINPSSNDDCRKRAEEVSSFIEF
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EviskchknkpgntsgktfwsQnsnpprawggQQQGRgsnvsgcgnnvsgcgncngrg
IQanisgrgralsrkyDnnfvApppvssrppleggmnQargdsAQHTAVQBFPDVEDD
VDNASEEENDSDALDDSDDLASDDVDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQ
INEPQRQWHCPACQNGPGALDWYNLHPLLAHARTKGARRVKLHRELLEVLEKDLQMRG
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/db_xref="GI:27754623"
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100.0%; Pred. No.
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Query Match 29.4%; Score 963; DB 6; Length 1878; Best Local Similarity 100.0%; Pred. No. 0; Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 696 ATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAGAACGTTCAGGGTGGTTATAGGCCT 755		JOURNAL Patent: WO 010591-A 2 25-JAN-2001; AVENTIS CROPSCIENCE S.A. (FR); INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (FR) Location/Qualifiers 1. 1878 //mol_type="unassigned DNA" /db_xref="taxon:3702" CDS /note="unnamed protein product"	1 AX078761 ION Sequence 2 from Patent ON AX078761 ON AX078761.1 GI:1315836 S Arabidopsis thaliana Eukaryota; Viridiplana Eukaryota; Viridiplana Spermatophyta; Magnolirosids; eurosids II; ICE 1 CE 1 CE 1 CE 1 CE 1 CRS Beclin, C. Elmayan, T.		Db 743 CAGATAAATGAACCACAGAGGCAGTGGCATTGTCCAGCTTGTCAGAACGGACCTGGTGCC 802 Qy 1407 ATCGATTGGTATAACCTGCACCCTCTACTAGCTCATGCGAGGACAAAAGGAGCTAGGCGA 1466
RESULT 6 BT004380 BT004380 BT004380 BT004380 DEFINITION Arabidopsis thaliana clone U20243 unknown protein (At5g23570) mRNA, complete cds. ACCESSION BT004380 VERSION BT004380.1 GI:28393932	1476 CATAGA 781 CATAGA 1536 CCTTGT 841 CCTTGT 1596 ATTGTC 901 ATTGTC 901 ATTGTC 1656 AAG 16 961 AAG 96	Db 601 AATAAGTGGTTCAAAAAAGTTCTTTGGCAGCTTGGATCGATC	. 1116 GCAAGAGGAGGTTCTGCTCAGCACACAGCTGTGCAGAGATTTTCCTGACGTGGAGGATGAT	Db 181 AAACTTIGGSTTICTCAGAATTCIGAATTCICCTTAGAACTTIGGAGTGGTCAGCAGCAGGG 240 Qy 936 AGAGGTAGCAACGTATCTGGGAGAGGAAACAATGTATCCGGGAGAGGGTAACGGCAATGGT 995 Qy 936 AGAGGTAGCAACGTATCTGGGAGAGGAAACAATGTATCCGGGAGAGGTAACGGCAATGGT 995 241 AGAGGTAGCAACGTATCTGGGAGAGGAAACAATGTATCCGGGAGAGGTAACGGCAATGGT 300 Qy 996 CGGGGCATTCAAGCTAACATATCTGGTCGGGAGAGGGTGAGCAGAAAGTATGATAAC 1055	Oy 756 GAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTCACAAGATGAT 815

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Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.
Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C.,
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamya, A., Kawai, J., Kim, C.J., Narusaka, M.,
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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NDSIKOIHERRDAKEENFEMLOOOERAKVVGOOOONINPSSNUDCRKKAEEVSSFIEF
ORKEMEEFVEEREMLIKDOEKKNEDMKKRHHEEIFDLEKEFDEALEOLMYKHGLHNED
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ઇ	B &	d dd	Query Match Best Local Matches 59	ORIGIN	리. : :	0	FEATURES			COMMENT	TITLE JOURNAL	REFERENCE AUTHORS	JOURNAL	TITLE	REFERENCE	VERSION KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION	RESULT 7	g dy	Db
1548 ATTTATGGGCAGTGGAAGGGTTTGGGTGAGGATGAAAAGGATTATGAAATTGTCTGGCCT 1607	1488 GCTGAAGTTTTAGAAAAGGATCTACAGATGAGAGGGGCATCTGTCATTCCTTGTGGTGAG 1547 	1428 CCTCTACTAGCTCATGCGAGGACAAAAGGAGCTAGGCGAGTTAAGCTCCATAGAGAATTG 1487 	/ Match 16.5%; Score 541; DB 8; Length 650; Local Similarity 99.8%; Pred. No. 1.9e-296; nes 591; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		feature	/organism="Arabidopsis thaliana" /mol_type="genomic_DNA" /mol_type="genomic_DNA"		graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genomics' (http://www.genomics.org.and.	to determine the genomic sequence Hanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a	PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly acquenced from the left or the right border) 12446565 2 (bases 1 to 650) 3 Balzergue,S.		Cha Cha	Eukaryota, Viridiplantae, Streptophyta, Embryophyta Spermatophyta, Magnoliophyta, eudicotyledons, core rosids, eurosids II, Brassicales, Brassicaceae, Ara	3	ATH528171 650 bp DNA linear PLN 29-MAR-2003 N Arabidopsis thaliana T-DNA flanking sequence, left border, clone 157008. A A A F S A I T		1656 AAG 1658 961 AAG 963	
	FEATURES		COMPLETA	TITLE JOURNAL	MEDLINE PUBMED REFERENCE AUTHORS	TITLE	AUTHORS	DEFECTION	KEYWORDS SOURCE ORGANISM	ACCESSION	ATH527741 LOCUS DEFINITION	RESULT 8	Qy 1 dd		· ⊔	ОУ 1 Db	Db 1	Db 1		оу 1
e 1.35 /organism="Arabidopsis thaliana" /mol_type="genomic DNA"		corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics	plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived segmences to form the respection of the right border to determine the genomic sequence flanking the insertion.	Direct Submission Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 9107 Evry cedex, FRANCE DOB was norfermed on DNA Evry credex.	22363535 12446565 2 (bases 1 to 45)	T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites	Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Leniniac I. Caboche M. and Locharny B.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	left border, T-DNA flanking sequence. Arabidopsis thaliana (thale cress) Arabidopsis thaliana	146F03. AJ527741 AJ527741 1 GI:26796001	ATH527741 45 bp DNA linear PLN 29-MAR-2003 Arabidopsis thaliana T-DNA flanking sequence, left border, clone		968 GTATGGCTTCCTTGCAACGAAGCAAGATCTGGACATATTCAATCAA	### OTTAGATAGAATTGCCTGGGGTCAGAAGCGCAGTATGTTTTCTGGAGGTGTTCGCCAACT 540	GAGCAGTGCCACTGGCTATTTGGAGGCCGAACGCCTCCACCGGGAGTTAGCTGAGATGGG	.788 TAGAGCACGCCATTCCTATGGTCCACAGGGCCATCGTGGGATGAGTGTTCTGATGTTTGA 1847	.728 GTAGTGGCTCGGCATGGGCAACCAAGAGCTGCTGGAATACTTCGACAAGTATGAGGCTCT 1787 	.668 TICHGTCTTTTACTTCTTTAATTTTTCTCTTGCATTCTACTGATCTTAGAATGTTACATT 1727	CCAATGGTCATCATGAATACTAGACTGGATAAGGACGATAACGATAAGGTGGAATTC	121 ATTTATGGGCAGTGGAAGGGTTTGGGTGAGGATGAAAAGGATTATGAAATTGTCTGGCCT 180 608 CCAATGGTCATCATGAATACTAGACTAGACTGATAAGGACGATAAGGTGGAATTC 1667

ORIGIN

misc_feature

Matches Query Match

Best Local

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NRS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Briren, B., Linton, L., Nusbaum, C., Lander, E., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Brown, A., Canarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, A., Chard, J., Chazellano, K., Diaz, J.S., Dodge, S., Faro, S., Cook, P., DeArellano, K., Diaz, J.S., Dodge, S., Faro, S., Cook, P., DeArellano, K., Collymore, A., Cook, A., Cook, P., Coo
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LITEUL SAUMHITSELLI,
SUBMITTED (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Genome 1,000 Charles Street, Ali,A., Allen,N., Anderson,S., Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Cook,A., Cooke,P., PitzGerald,M., Gage,D., Galagan,J., Farco,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Garaham,L., Grand-Pierre,N., Hafez,N., Gardyna,S., Gord,S., Garaham,L., Johnson,R., Jones,C., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Kantt,A., Karatas,A., Kells,C., Landers,T., Levine,R., Kantt,A., Karatas,A., Kells,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Menthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Morbu,C., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Morman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
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Mus musculus clone RP24-329L16,
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Birren, B., Nusbaum, C.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/db xref="taxon:3702"
/clone="146F03"
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Center clone name: 329_L_16
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Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Pierre, C., Connect, C., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 31, 2002 this sequence version replaced gi:22381142. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Submitted (31-OCT-2002) Whitehead Institute/MIT Center for Genome Center: Whitehead Institute/ MIT Center for Genome Research

Contact: sequence submissions@genome.wi.mit.edu Web site: http://www-seq.wi.mit.edu

Center clone name: 329 L 16

------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 169312 bases at least 040
Consensus quality: 170102 bases at least 030
Consensus quality: 170295 bases at least 020
Consensus quality: 170295 bases at least 020 Insert size: 163000; agarose-fp
Insert size: 170365; sum-of-contigs
Quality coverage: 17.6 in Q20 bases; agarose-fp
Quality coverage: 16.8 in Q20 bases; sum-of-contigs

ACCESSION VERSION

DEFINITION AC102284/c RESULT 9

SOURCE

ORGANISM

KEYWORDS

REFERENCE

REFERENCE

AUTHORS JOURNAL TITLE AUTHORS

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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/db_xref="taxon:10090"
/clone="RP24-329L16" organism="Mus musculus" 76853: contig of 76853 bp in length
76953: gap of 100 bp
78949: contig of 1996 bp in length
79049: gap of 100 bp
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150873: gap of 100 bp
170765: contig of 19792 bp in length.
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REFERENCE

AUTHORS

TITLE JOURNAL

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RESULT 10
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AUTHORS
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Burton, J.
Direct Su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidi
Aphidoidea; Aphididae; Macrosiphini; Uroleucon.
1 (bases 1 to 554)
Moran, N.A., Kaplan, M.E., Gelsey, M.J., Murphy, T.G. and Sch
Phylogenetics and evolution of the aphid genus Uroleucon
mitochondrial and nuclear DNA sequences
Syst. Entomol. 24 (1), 85-93 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF057056 Inear INV 19-DEC-200 Uroleucon erigeronensis NADH dehydrogenase subunit 1-like protein (ND1) gene, partial sequence; mitochondrial gene for mitochondrial
                                                                                                 BX004860.1 GI:26985650
HTGS PHASE1; HTGS DRAFT.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                               BX004860 101080 bp
Danio rerio clone BUSM1-144B24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-APR-1998) Ecology and Evolutionary Biology,
University of Arizona, Biological Sciences West, Tucson, Arizona
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Moran, N.A., Kaplan, M.E., Gelsey, M.J., Murphy, T.G.
                                                                                                                                                                                 pieces.
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                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                               (bases 1 to 101080)
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/db_xref="taxon:87314"
<1. .>554
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ND1"
/note="similar to NADH dehydrogenase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="ND1"
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100.0%; Pr
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WORKING DRAFT SEQUENCE,
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Aphidiformes;
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4 unordered
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zface@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
------ Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-DEC-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coverage: 5.56x in Q20 bases; agarose-tp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: dZ144B24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: SC
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                                                                                                                                   AAATGAAAACAAAATCAAACTGA 118
                                                                                        AAATGAAAACAAAATCAAACTGA 39769
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071 34170: gap of 100 bp
171 67630: contig of 33460 bp in length
631 67730: gap of 100 bp
731 81714: contig of 13984 bp in length
715 81814: gap of 100 bp
815 101080: contig of 19266 bp in length.
Location/Qualifiers
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vector_side:right"
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                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment:00119
fragment_chain:1
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Fragment_chain:1"
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment:00417
fragment_chain:1
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/db_xref="taxon:7955"
/clone="BUSM1-144B24"
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ive 0; Mismatches
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AL845510

101241 bp

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VRT 30-JAN-2003

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VERSION
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Best Local Similarity
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names beginning 'Dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www/Projects/D_rerio/fishmask.shtml BUSMI-132M23 is from a Zebrafish PAC library
                                                                                                                                                                                                                                                                        39751 AAATGAAAACAAAATCAAACTGA 39729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 101241)
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ACL107028 126716 bp
HOmo sapiens 3 BAC RP11-547K2 (R
BAC Library) complete sequence.
AC107028
AC107028.5 GI:28006935
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="BUSM1-132M23"
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/clone_lib="BUSM1"
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Pred. No.
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Ostariophysi;
                                                                                                            Park Cancer
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
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Submitted (14-JAN-2002) Human Genome Sequencing Center, Department Submitted (14-JAN-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
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Submitted (30-APR-2002) Human Genome Sequencing Center, Department Submitted (30-APR-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                 Submitted (29-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                 Submitted (02-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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Submitted (29-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 29, 2003 this sequence version replaced g1:20340431.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Submitted (29-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Navlor Plaza, Houston, TX 77030, USA
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Submitted (30-MAY-2002) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Bavlor Plaza, Houston, TX 77030, USA
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Direct Submission
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                   complement(1..3011)
/note="overlaps bases 1.
/function="clone overlap"
                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                        Location/Qualifiers
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1 (bases 1 to 152345)
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BX005128.4 GI:37518236
                                                                              Danio rerio (zebrafish)
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Only a small overlap as described above.

Only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequencing problems, such 30); an attempt was made to resolve all sequencing problems, such 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least as compressions and repeats; all regions were covered by at least as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the rare assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given beginning 'dar' (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dar' were identified by Rick Waterman (Stephen Johnson lab, Washu). For were identified by Rick Waterman (Stephen Johnson lab, washu).
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Submitted (03-OCT-2003) Wellcome Trust Sanger Institute, Hinxton, Submitted (03-OCT-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
Zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 5, 2003 this sequence version replaced gi:30141705.
On Oct 5, 2003 this sequence version replaced gi:30141705.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
CH211-129H14 is from a CHORI-211 BAC library
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                                                                                                                                      AC048381.3 GI:8084282
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180925)
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sapiens chromosome 3 clone RP11-547K2 map 3, WORKING DRAFT
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8381
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-129H14"
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TITLE
JOURNAL
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Barren,B., Linton,L., Musbaum,C., Lander,B., Burkett,G.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boyuslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Boyuslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Campopiano,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Galagan,J., Gardyna,S., Ginde,S., Jones,C., Kann,L., Karatas,A.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Howland,J.C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Klein,J., LaRocque,K., Lamazares,R., Maddonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McCarthy,M., McEwan,P., McGurk,A., Mraddonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., Mraddonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., Mraddonald,P., McPheeters,R.,
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McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,R., McPheeters,R.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,R., McPheeters,R.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,R., McCarthy,M., McDan,P., McCarthy,M., McC
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RES (Dases 1 to 18925)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Estar, B., Linton, L., Barra, N., Bactar, V., Beda, F., Anderson, S., Baldwin, J., Barra, N., Bactar, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Boguslavkiy, L., Boukhgalter, B., Colangelo, M., Collins, S., Campopiano, A., Cocke, P., Dewar, K., Diwar, K., Diaz, J.S., Collymore, A., Cocke, P., Dewar, K., Dewar, K., Diaz, J.S., Collymore, A., Cocke, P., Dewar, C., Marcha, P., Graham, L., Garadan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Garadan, J., Grant, G., Hagos, B., Heford, A., Horton, L., Grand, Pierre, N., Grant, G., Hagos, B., Handers, T., Lehozzky, J., Klein, J., Lancoque, K., Lamazares, R., Landers, T., Lehozzky, J., Klein, J., Lancoque, K., Lamazares, R., Landers, T., Lehozzky, J., Klein, J., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarnan, K., McPheeters, R., McCarnan, K., McPheeters, R., McCarnan, C., McReynond, C., Miranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Comnor, T., O'Donnell, P., Marquis, C., Pitare, N., Olivar, T.M., Olivar, T.M., Olivar, T.M., McCarnan, K., Pierre, N., Pierre, N., Sender, B., Schauer, S., Severy, P., Rothman, D., Pierre, M., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Toylor, S., McCart, S., McCarnan, A., Talamas, J., Voll, R., Voll, R., Voll, M., Mison, B., Mu, X., Wyman, D., Ye, W.J., Norman, C., Simmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-AUG-2002) whitehead Institute/MIT Center for Genome Submitted (24-AUG-2002) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced 91:7770638.

On May 25, 2000 this sequence version replaced 91:7770638.

All repeats were identified using RepeatMasker: html http://ftp.genome.washington.edu/RM/RepeatMasker.html http://ftp.genome.washington.edu/RM/RepeatMasker.html http://ftp.genome.center
Center clone name: 547 K 2

------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Assembly guality: 158029 bases at least Q40
Consensus quality: 168695 bases at least Q20
Consensus quality: 173285 bases at least Q20
Consensus quality: 173285 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
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RP11-547K2
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NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
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Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
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1110: gap of
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116971: contig of 7986 bp in length
117071: gap of 100 bp
126718: contig of 9647 bp in length
126718: gap of 100 bp
137354: contig of 10536 bp in length
137454: gap of 100 bp
137454: gap of 100 bp
146943: contig of 9489 bp in length
147043: gap of 100 bp
157785: contig of 10742 bp in length
157785: contig of 10742 bp in length
157885: gap of 100 bp
180925: contig of 23040 bp in length.
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Aas61413 Human gen	Abl70450 Chemicall	Abk31481 Signal tr	Abl34150 Human imm	Abl32823 Human imm	Aas46376 Tumour su	Abz10216 Haematopo	Abz10070 Haematopo	Adb54169 Pretreate	Adb54297 Pretreate	Aba20651 Human ner	Aca23079 Prokaryot	Aal25105 Human bre	Abt07654 Human bre	Add48892 Rat gene	Add47852 Rat gene	Add47853 Rat gene	Abk48300 Human inh	Abq30108 Oligonucl	Abq30109 Oligonucl	Aah93017 Human inf	Aax27594 Nucleotid

ALIGNMENTS

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FT exon exon exon AAF25373; 16-JUL-1999; 99FR-00009417. 26-JAN-2000; 2000FR-00001006. WO200105951-A2. SGS3 gene; post-transcriptional inactivation; RNA degradation; viral resistance; resistance; fatty acid content; protein content; ss. AAF25373 standard; (AVET) AVENTIS CROPSCIENCE SA. (INRG) INST NAT RECH AGRONOMIQUE. 13-JUL-2000; 2000WO-FR002052. 25-JAN-2001. intron intron exon intron intron exon Arabidopsis thaliana. Genomic sequence of the Arabidopsis SGS3 gene 15-MAY-2001 (first entry) /*tag= e 2380..2481 /*tag= f 2482..2648 /*tag= g 2649..2738 a /*tag= b 1732...2 Location/Qualifiers 696. .1658 1732. .2023 /*tag= c 2024. .2134 /*tag= d /*tag= d 2135. .2379 DNA; 3275 ВP

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Overexpression of SGS3 results in plants with increased resistance to Overexpression of SGS3 results in plants with increased resistance to Viruses, while inactivation of SGS3 in transgenic plants (e.g. by viruses, while inactivation of SGS3 in transgenic plants (e.g. by increases the level of the transgene product. This product may e.g. increases the level of the transgene product. This product may e.g. inspart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active, e.g. a immunoclability or interference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene
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                                                                   expression.
                                                                                    New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene
                                                                                                                                                        WPI; 2001-159529/16
P-PSDB; AAB31798.
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26-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the Arabidopsis SGS3 polypeptide.
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viral resis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene expression.
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26-JAN-2000; 2000FR-00001006.
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resistance; resistance; fatty acid content; protein content;
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Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tu cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TX UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 6 A; 4.C; 7 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beclin C,
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26-JAN-2000; 2000FR-00001006.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF25371;
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                                                                                                                                                            Human chemically pretreated gene sequence #62 strand 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 ABK40041 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 6136
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                                          TXNRD1;
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KW hear
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Best Local S
Matches · 22
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Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;

Human chemically modified disease associated gene SEQ ID NO 117.

ABN80100

ABN80100 standard; DNA; 6301 BP

Similarity

Conservative 0;

0.7%; Score 22; DB 100.0%; Pred. No. 12;

6; Length 6136;

Mismatches

0

<u>.</u>

Gaps

0

15-JUL-2002

(first entry

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The invention relates to a nucleic acid comprising a sequence at least 18 CC bases in length of a segment of the chemically pretreated DNA of genes CC associated with pharmacogenomics according to one of the sequences of the CC genes ALDH6 (NM 000693), CYP11A (NM 000781), CYP11B1 (NM 000979), CCLN (NM 000776 and NM 017460), DPYD (NM 000110), EPHX2 (NM 001979), CCLN (CC (NM 01990), NM 019901, NM 019902, NM 019902, NM 019982, NM 019988, NM 019899) and CC their complementary sequences, or a sequence (S1) chosen from 87 CC sequences and their complements. The chemical pretreatment is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an oligonucleotide or a CC peptide nucleic acid (PNA)-oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with CC pharmacogenomics and their complements, arranged in an array for canalysing diseases associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The coligomers may also be used as PCR princers. The set of 87 nucleic acids and their complement. Nuclei The set of 87 nucleic acids cand their complement is useful for diagnosis and therapy of solid cont form part of the princed specification, but was obtained in CC electronic format directly from MIPO at CC electronic format directly from MIPO at CC electronic format directly from MIPO at two controls and the control of the set of the sequences.
Sequence 6136 BP; 1661 A; 69 C; 1415 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
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01-SEP-2000; 2000DE-01043826
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0 U; 0 Other;
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RESULT 7
ABL33241
ID ABL3
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AC ABL3
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DT 26-P
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DT 26-P
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Huma
KW Huma
KW Ant:
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                                                                                                                                                                                                                                                                                                                                                                                 CC sequences (ABN7996-ABN80333) or their complements. The invention is sequences (ABN7996-ABN80333) or their complements. The invention is CC useful for the diagnosis or therapy of diseases associated with congenity of the diseases related to homeobox containing CC development genes, in particular disease related to homeobox containing CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes CC associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the CC histone deacetylation, Currarino syndrome, diseases related with the CC disjomers specific to each of the genes are useful for detecting the CC (II) and their complementary sequences, as primer oligonuclectides for the amplification of the 350 sequences, (II) and/or their complements and CC the amplification of the 350 sequences, (II) and/or their complements and constant probes for detecting the cytosine methylation state and/or their sequences for detecting the cytosine methylation state and/or patent did not form part of the printed specification but is based on constant of the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with development genes such of a segment of chemically pretreated
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                                                                                                                                                                                                                                                                                                                                                             Sequence 6301 BP; 1787 A; 59 C; 1247 G;
             Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                     Human immune system associated gene SEQ
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22; Conserv
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                                                                                                                                                                             standard; DNA;
                                                                                                                                                                                                                                                  TAGTATTTTGTTTTTTTTGGT 3750
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2000DE-01043826.
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                                                                                                                   (first
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      eye
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       disease;
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            anaemia;
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片 5

02-JUL-2001; 2001WO-EP007537

03-JAN-2002.

WO200200928-A2

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RESULT 8
ABL32
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ABL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9888 BP; 2830 A; 160 C; 2148 G; 4750 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisposoriatic; antinflammatory; cancer; eye disease; arreriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; neurofibromatosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL32509;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGTATTTTGTTTTTTTTTGGT 3163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGTATTTTGTTTTTTTTGGT
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2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO 1214; 32pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 6048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated gene SEQ ID NO: 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                            epilepsy;
bowel disease;
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RESULT 9
ABL3207
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune system disease; cytosine methylation; antiasthmatic; antiatreriosclerotic; antianzemic; cytostatic; nootropic; neuroprotective; anti-HU; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirheumatic; antiarchritic; antidiabetic; antipsoriatic; antimplammatory; cancer; eye disease; arteriosclerosis; anaemia; antimplammatory; cancer; eye disease; arteriosclerosis; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid
diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; antiarteriosclerotic; antianae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-130909/17
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01-SEP-2000; 2000DE-01043826.
                                                                                               01ek
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                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                               03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; cancer; eye diseas(
acute myeloid leukaemia; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
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                                               WPI; 2002-130909/17
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                                                                                                                                            EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 482;
                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment of of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32pp +
                                                                                            Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease; AIDS; epilepsy;
tis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified gene, with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Nucleic acid comprising fragment of chemically modified gene, useful

for

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RESULT 10
AAS46448
ID AAS466
XX AAS46
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Matches 21
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                                                                       The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 are missing from the sequence listing) sequences (Ss) and sequences 500 are missing from the sequence listing) sequences (Ss) and sequences
                                                                                                                                                                                                                                                                                                  Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzin diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2000; 2000DE-01013847

06-APR-2000; 2000DE-01019058

07-APR-2000; 2000DE-01019173

30-JUN-2000; 2000DE-01032529

01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                 Claim 1;
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                            complementary to (Ss). The nucleic acid may be a peptide nucleic acionigomer (PNA) of at least 9 nucleotides and may form part of a set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200168912-A2
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Pred. No.
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polymorphism; SNP;
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ABN80176
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Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN80176 standard; DNA; 13453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
The invention relates to a nucleic acid (I) comprising a sequence a least 18 bases in length of a segment of chemically pretreated DNA of genes associated with development selected from 87 genes listed specification such as ACCDN, ADFN, or AFD1 and comprising one of 35 sequences (ABN79984-ABN80333) or their complements. The invention is
                                                                                                                                                                                                                                          Olek A,
                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP007536.
                                                                                                                                           Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                             WPI;
                                                                                               Claim 1; SEQ ID NO 193;
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2000DE-01043826.
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a invention also encompasses expression vectors and host cells comprising CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or binds to the protein, and a biochip comprising CA nucleic acid or oncogenic retroviruses, which insert into the genome of the host organism oncogenic retroviruses, which insert into the genome of the host organism oncogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic trans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic retrans-acting viral genes, meaning that cancer incidence is a pathogenic viral genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant nucleic acid encoding carcinoma useful for preparing compositions for treating c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morris
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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                                                                                                                                                                                   nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
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23-0CT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 304; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancers,
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                                                                                                                                  Sequence 52302 BP;
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel recombinant nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant nucleic acid, useful for treating carcinomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-DEC-2001; 2001WO-US051291.
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C Local Simulation 21;
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                                                                    Length 52302;
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                          Hybridisation assay; genetic mapping; gene of protein identification; signal transduction
                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 71849.
                                                                                                                                                                                                             AAC52596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomass. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA; secreted; transmembrane; intracellular; ds.
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                                                                                                                                                                                                                                                             AAC52596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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JOURNAL COMMENT REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS AQ959658/c LOCUS ACCESSION DEFINITION TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 693) Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based Contact: Xiaoying Lin The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: at@tigr.org For addtional information, see http://www.tigr.org/tdb/at/at.html polymorphisms Unpublished (2000) Arabidopsis thaliana (thale cress) Arabidopsis thaliana GSS survey sequence. AQ959658 AQ959658 693 bp DNA linear GSS 28-JAN-2000 LEREMAITFB LERE Arabidopsis thaliana genomic clone LEREM21, genomic AQ959658.1 GI:6787359

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/mol_type="genomic DNA"
|strain="LANDSBERG ERECTA"
|db_xref="taxon:3702"
|clone="LEREM21"
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/note="Organ: Leaf; Vector: pUC19JK; Total genomic
/note="Organ: Leaf; Vector: pUC19JK; Total genomic
sheared to 0.6-0.8 Kbp before ligation."
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Unpublished (2000)
Contact: Xiaoying Lin
Contact: Xiaoying Lin
Por Institute for Genomic Research
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1 (bases 1 to 606)

Buell, C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.

Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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                                         GAACGGACCTGGTGCCATCGATTGGTATAACCTGCACCCTCTACTAGCTCATGC 1444
                                                                                                                                                    radcitigicantcaagcagaraaargaaccacagaggcagregecatregrecagerrepro
                                                                                                                                                                                                                                                                                                     <u>AAAGAGCCATGGATCACGAAAGCAGAATAAGTGGTTCAAAAAAGTTCTTTGGCAGCTTGGA</u>
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/mol_type="genomic DNA"
/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
/clone="LEREN21"
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/clone lib="LERE"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was
sheared to 0.6-0.8 Kbp before ligation."
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Pred. No. 3.3e-256;
0; Mismatches 0;
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Matches 521;
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Best Local Similarity
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carrinci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibarah
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Motoaki Seki
Plant Functional Genomics Research Group
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AU236368.1 GI:19875537
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AU236368

RAFL14 Arabidopsis thaliana cDNA clone RAFL14-93-K05 5',
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                                                                                                        CAGCAAGGGAGAGGTAGCAACGTATCTGGGAGAGGAAACAATGTATCCGGGAGAGGTAAC
                                                                                                                                                                                                                                                                 CAAGATGATGGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAAAC
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GGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCAGAAAG
                         GGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCAGAAAG
                                                                                                                                                                                                                                        CAAGATGATGGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAAAC
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                                                                                                                                                                                                  ACTTCTGGAAAAACTTGGGTTTCTCAGAATTCGAATCCTCCTAGAGCTTGGGGTGGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RAFL14-93-K05"
/tissue_type="root"
/lab_host="DH10B"
/clone_lib="RAFL14"
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/db_xref="taxon:3702"
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Pred. No. 1.1e-249;
0; Mismatches 0;
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Best Local S
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1 (bases 1 to 613)
1 (bases 1 to 613)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feeldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr., Ro
Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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LERGX20TF LERG Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: TF
Class: shotgun
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The Institute for Genomic
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                                                                                                                                                                                                                                                            Similarity
                 CTGGCTTCTTCACAAGATGATGGAGGAGAGAGGAAGAACAAGAAC
                                                                                                                                       TGGTGGCTATAGGTTGTAAAAATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAAGAAC
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CTGGCTTCTTCACAAGATGATGGAGGAGGTGGGAGGTCATTTCCAAGAAGAACAAGAAC
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/note="Organ: Leaf; Vector: pUC19JK; Total
sheared to 0.4-0.7 Kbp before ligation."
                                                                                                                                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
|mol_type="genomic DNA"
|strain="LANDSBERG ERECTA"
                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:3702"
clone="LERGX20"
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Pred. No. 3.8e-241;
0; Mismatches 2;
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Rockville,
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hes 451; Conservative
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              1682 TCTTTAATTTTTCTCTTGCATTCTTACTGATCTTAGAATGTTACATTGTAGTGGCTCGGCA 1741
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNSOOP9H 457 bp DNA linear GSS 28-JUN-1999
Arabidopsis thaliana genome survey sequence T7 end of BAC F8G21 of
IGF library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                                                                                                                                                          Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                 survey sequence.
AL084227
AL084227.1 GI:5
                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                Genoscope
                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                    Salanoubat, M., Choisne, N., Artiguenave, F., Samson, D., Saurin, W., Weissenbach, J. and Qu
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                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia"
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                /clone="F8G21"
/clone_lib="IGF"
/note="end : T7"
                                                                                                                                                      /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:5285367
                                                  0;
                                                               Score 451;
Pred. No.
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                                                                1.6e-214;
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                                                                           Length 457;
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AU227277
AU227277.1 GI:
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Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                             Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
Email: mseki@rtc.riken.go.jp
An Arabidopgis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998) cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                             (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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/clone_lib="RAFL14"
/note="Site_1: BamHI; Site_2: SalI"
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/db_xref="taxon:3702"
                                                                                                                                                                                                                organism="Arabidopsis"
                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                        Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillnan, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and
                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 548)
                                                                                                                                      4633 World Parkway Circle, St. Louis, MO 63134, USA Tel: 877-577-2733
                                                                                                                                                                                                                Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
                                                                                                                                                                   Genome Systems, Inc., a wholly owned Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI999551.1 GI:5846456
                                                                                                                                                                                                Contact: David Smoller, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAAGTTTCTTTGCTTTTGGTATGTCGGAAAGTAGGAGATCTGAGAGACTCCATT
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                                                                                                                        314-427-3324
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                                                                                        service@genomesystems.com
Location/Qualifiers
/db_xref="taxon:3702"
/clone="701556368"
                              /mol_type="mRNA"
/cultivar="Columbia Col-0"
                                                         organism="Arabidopsis thaliana"
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                                                                                                                                                                                   subsidiary of Incyte
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                              FEATURES
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                                                                                                                                      JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                            ORGANISM
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                                                                                                                         PUBMED
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2781 GATGGACGAGTTTGTGGAAGAGAGGGGAGATGCTGATAAAAGATCAAGAGAAGAAGAAGATGGA
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 380)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV525508 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone APD25d02R 5', mRNA sequence AV525508
                                                                                                                                                                                    The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV525508.1 GI:8685036
EST.
                                                                                                                                                                                                                                                   Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
                                                                                                                    Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                  10907847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATTTTAGTAGACGGATCTAAGGAAGCATTAA 12
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/note="Vector: pSPORT; Site_1: NotI; Site_2: SalI; cDNA
library was derived from untreated rosette tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with ferrilizer. CDNA synthesis was initiated
using a NotI-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to SalI adaptors, digested with NotI,
size-selected, and cloned into the NotI and SalI sites of
the pSPORT vector."
                                                                                           Location/Qualifiers
organism="Arabidopsis/mol_type="mRNA"
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100.0%; Pred. No. 8.8e-156;
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to six-week
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AUTHORS
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VERSION
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AQ010650.1 GI:3165927
GSS.
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1 (bases 1 to 290)
1 (bases 1 to 290)
1 (bases 1 to 290)
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                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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primer: M13 Reverse
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/db_xref="taxon:3702"
/clone="APD25d02R"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana aboveground organs two six-week old"
                             rounsley@tigr.org
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High quality sequence stop:
Location/Qualifiers
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Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
AQ959659
AQ959659.1 GI:6787360
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                             Unpublished (2000)
Contact: Xiaoying Lin
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                              Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For addtional information,
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/note="Vector: BeloBACII; Site_1:
produced by Thomas Altmann"
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/strain="Columbia"
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'clone="F27C8"
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organism="Arabidopsis thaliana"
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    Li,Y.,
Direct
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                                                                                                                                                                             A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
                                                                                                                                                                                                                                                      Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence.
                                                             Unpublished
                                                                             for flanking sequence
                                                                                                                    Rosso, M.,
                                                                           osso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) relating sequence tag based reverse genetics
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(bases 1 to 536)
Y., Rosso,M., Strizhov,N.
ect Submission
                                                                                                                                                                                                                                        Weisshaar, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: Leaf; Vector: pUC19JK; Total sheared to 0.6-0.8 Kbp before ligation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="LERE"
                                                                                                                                                                                                                                                                                                                                                                                                                 GI:24402266
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No. 3.8e-125;
                        and
                        Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
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KEYWORDS
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Best Local Similarity
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                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 619)
1 (bases 1 to 619)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
BNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV566465 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ244b06F 3', mRNA sequence.
Contact: Erika Asamizu
The First Laboratory for Plan
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Genomics program designated 'GABI'. Information on line availability can be found at a http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone MQM1. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                10907847
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ilarity 100.0%;
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/clone=lib="Arabidopsis thaliana T-DNA insertion lines"
/clone lib="Arabidopsis thaliana foliana fol
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/mol_type="genomic DNA"
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Pred. No. 1.4e-104;
0; Mismatches 0;
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 bp DNA linear GSS 30-JAN-200 SALK 039005 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 039005, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R. A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                            Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Pax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis Genome Unpublished (2001)
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                                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g23570.
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/clone_Tib="Arabidopsis_thaliana_green_siliques_Columbia"
/note="Vector: pBluescriptII_SK-; Site_1: EcoRI; Site_2:
KhoI"
                                                                                                                                                                                                                                                                                                            ecker@salk.edu
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/strain="Columbia"
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/mol_type="genomic_DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_039005"
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Arabidopsis thaliana T-DNA flanking
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Submitted (01-UUI_2003) Weisshaar B., Max-Planck-Institut fuer Submitted (01-UUI_2003) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone MQM1. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the Germa Plant Genomics program designated 'GABI'. Information on line plant denomics program designated 'GABI-Kat'. http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                  Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and We A new Arabidopsis thaliana T-DNA mutagenised population for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                    A pipeline for automated (flanking sequence tags) transformed lines
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                                                                                                                                                                                          3 (bases 1 to 395)
Strichov, N., Li, Y., Rosso, M. and Weisshaar, B.
Direct Submission
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
each if the resultant fragment for each line was
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
the site of insertion. Details of the protocols.html"
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pred. No. 1.9e-80;
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GK-547E01-020631,
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(GABI-Kat)
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/organism="Arabidopsis thaliana" /mol type="genomic DNA" /strain="Columbia 0"

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RESULT 15
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                                                                                                                                                                                                                                                                                                                   Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 197)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zhmmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 bp DNA linear GSS 03-OCT-200 SALK_001394 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_001394, genomic survey sequence.

BH169457
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Unpublished (2001)
Contact: Joseph R. Ecker
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Arabidopsis thaliana
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                                                                                                                                                                                                                      TDNA tagged
                                                                                                                                                                                                                                                                                               ecker@salk.edu
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/clone="SALK_001394"
/clone_lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
                                                                         /mol_type="genomic_DN
/strain="Columbia_0"
/db_xref="taxon:3702"
                                                                                                                                             organism="Arabidopsis thaliana"
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Pred. No. 2.1e-73;
0; Mismatches 1;
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TERSION

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Query Match elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" each of which contains one or more TDNA insertion Score 153; DB 28; Pred. No. 8.3e-65; Length 197; can

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Similarity

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Ś Ś Ş 밁 밁 Matches 121 865 805 745 153; 5 ACACTTCTGGAAAAACTTGGGTTTCTCAGAATT CACAAGATGATGGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAA GTTATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTT GTTATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTT CACAAGATGATGGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAA ACACTTCTGGAAAAACTTGGGTTTCTCAGAATT 153 Conservative 0 Mismatches 897 Indels 0 Gaps 120 864 804 60 0

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Match
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4 US-09-615-192A-27

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3 US-08-669-161A-29

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Sequence 120, App	Sequence 120, App	Sequence 49, Appl	Sequence 49, Appl	Sequence 49, Appl	Sequence 49, Appl	Sequence 25, Appl	Sequence 2618, Ap	Sequence 15, Appl	Sequence 8, Appli	Sequence 14, Appl	•	Sequence 10, Appl	Sequence 7, Appli	Sequence 6, Appli	Sequence 12, Appl	Sequence 11, Appl	Sequence 1, Appli

ALIGNMENTS

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Sequence 1, Application US/09736734

Patent No. 6537815

GENERAL INFORMATION:

APPLICANT: ROMEO, TONY
TITLE OF INVENTION: ESCHERICHIA COLI CSRB GEI
TITLE OF INVENTION: ESCHERICHIA COLI CSRB GEI
TITLE OF INVENTION: THEREBY, AND METHODS OF
FILE REFERENCE: 316082002001

CURRENT FILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 09/112,584
PRIOR APPLICATION NUMBER: 69/12,584
PRIOR APPLICATION NUMBER: 60/052,372
PRIOR APPLICATION NUMBER: 60/052,372
PRIOR FILING DATE: 1997-07-11

NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 654
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-112-584-1
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US-09-112-584-1/c
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APPLICANT: University of No. 6228638th Texas
APPLICANT: University of No. 6228638th Texas
TITLE OF INVENTION: THE ESCHERICHIA COLI CSRB GENE, RNA ENCODED THEREBY,
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 31608200200
CURRENT APPLICATION NUMBER: US/09/112,584
CURRENT FILING DATE: 1998-07-09
EARLIER APPLICATION NUMBER: US 60/052,372
EARLIER APPLICATION NUMBER: US 60/052,372
EARLIER FILING DATE: 1997-07-11
NUMBER OF SEQ 1D NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
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Patent No. 6228638
GENERAL INFORMATION:
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Best Local Similarity
Matches 20; Conserv
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US-09-169-789-109
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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US-09-615-192A-109/c
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Best Local Similarity 100.0%;
Matches 20; Conservative
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LENGTH: 481
                                                                                                                                                                                                                                                                                                                                                         Patent No. 6653528
GENERAL INFORMATION:
APPLICANT: Blokeberg, Leonard N.
APPLICANT: Havukkala, Ilkka
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APPLICANT: Bloksbe
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  Query Match
                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 109
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                                                                                                                                                                                                                   TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin (FILE REPERENCE: 11000.103c2 CURRENT APPLICATION NUMBER: US/09/169,789 CURRENT FILING DATE: 1998-10-09 EARLIER APPLICATION NUMBER: US 08/975,316 EARLIER FILING DATE: 1997-11-21
                                                                                                                                                        EARLIER APPLICATION NUMBER: US 08/713,000 EARLIER FILING DATE: 1996-09-11 NUMBER OF SEQ ID NOS: 185
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                                                           ORGANISM: Eucalyptus grandis
                                                                                  LENGTH: 481
TYPE: DNA
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mes 19; Conservative (
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Havukkala, Ilkka
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100.0%; Pred. No.
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; Sequence 27, Application US/09615192A
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                                                                                                                                                                        RESULT 6
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                                                          GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
APPLICANT: Havukkala, Ilkka
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Matches 19; Conserva
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                TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin FILE REFERENCE: 11000.1003C4U
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 base pairs
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CURRENT APPLICATION NUMBER: US/09/615,192A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR TITLE OF INVENTION: THE MODIFICATION OF PLANT NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOUTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 495 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-269-0563
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                                                                                                                                                                                                                                                                 769 TGGTTCAAGGTTTGGCAGG 787
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                                                                                                                                                                                                                                                                                       Similarity 100.0%; Preq. No. -. Similarity 0; Mismatches
                                                                                                                                                                                                                              TGGTTCAAGGTTTGGCAGG 466
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; Pred. No.
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; Mismatches
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CURRENT FILING DATE:

2000-07-12

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CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: US 08/713,000
EARLIER FILING DATE: 1996-09-11
NUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Thiches 19; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-27
                                                                                                                                                                                                                                                 US-08-484-105-19
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Matches
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EQ ID NO 27
LENGTH: 495
TYPE: DNA
ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                               Sequence 19, Appli
Patent No. 5589341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6653528 GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Materials and Methods TITLE OF INVENTION: Modification of Plant FILE REFERENCE: 11000.1003c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bloksberg,
APPLICANT: Havukkala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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mes 19; Conserv
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                                                                                                                                                                                                                                 Application US/08484105
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LAURENSON, PATRICIA
HERSKOWITZ, Ira
LI, Joachim J
GAVIN, Kimberly
VENTION: ORIGIN OF REPLICATION COMPLEX GENES
                                                                                          RINE, Jasper
FOSS, Margit
McNALLY, Francis J
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                             BELL, Stephen P
KOBAYASHI, Ryuji
                                                                                                                                                                               STILLMAN, Bruce
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00.0%; Pred. No.
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24;
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Matches
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                            APPLICANT:
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REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
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NAME: Osman Ph.D., Richard Aron
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APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                              APPLICANT:
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                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 19; Conserv
                                                   ZIP: 94111-4187
                                                                 COUNTRY:
                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                ADDRESSEE:
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                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 494-8771
                                                                                                                                                                             GAVIN, Kimberly
JENTION: ORIGIN OF REPLICATION COMPLEX GENES
                                                                                                                                                                                                                                                                                        RINE, Jasper
                                                                                                                                                                                                                                                                                                         KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 19; DB llarity 100.0%; Pred. No. 24 Conservative 0; Mismatches
                                                                                                                                                                                                                          HERSKOWITZ,
                                                                                                                                                                                                                                                        FOSS, Margit
McNALLY, Francis
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277..1365
                                                                                                                                                                                                                                         LAURENSON, Patricia
                                                                                                                                                                                                                                                                                                                                          STILLMAN, Bruce
                                                                                                                                FLEHR, HOHBACH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 494-8700
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                                                                                                                 TEST, ALBRITTON & HERBERT
er, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
. 24;
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                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-377-557-9
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                                                                           RESULT 11
US-09-041-075A-4
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                                                                                                                                                                                                                                                                                                              SEQ ID NO 9
LENGTH: 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 494-8771
TELEPAX: (415) 494-8771
TELEX: 910 277299
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                            Sequence 4, Application Patent No. H002022
Patent No. H002022
GENERAL INFORMATION:
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Emil M. Jr.
APPLICANT: NUNENTION: Amino Acid Decarboxylases
FILE REFERENCE: BB-1237
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/377,557
CURRENT FILING DATE: 1999-08-19
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                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/099,493
EARLIER FILING DATE: September 8, 1998
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Office 97
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 19; DB 1;
Local Similarity 100.0%; Pred. No. 24;
28 19; Conservative 0; Mismatcher
                                                                                                                                                                                                   Local Similarity hes 19; Conserv
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                                                                                                                                         1844 TTTTTTTTGGTAAATTT 1826
                                                                                                                                                           3152 TTTTTTTTTGGTAAAATTT 3170
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                                                            Application US/09041075A
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 Heidler, Steven A
Radding, Jeffrey A
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277..1365
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                                                                                                                                                                                                                       0.6%; Score 19; DB 3; 100.0%; Pred. No. 24;
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SEQ ID NO 4
LENGTH: 2000
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US-09-041-075A-6
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SEQ ID NO 6
LENGTH: 2000
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                                                                                                                                                                                                                    RESULT 13
US-09-595-684B-30
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CURRENT FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/043,591
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Heidler, Steven A
APPLICANT: Radding, Jeffrey A
TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
FILE REFERENCE: X-11242 Sequence Let
Patent No. H002022
Patent No. H002022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Patent No. H00202
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Best Local Similarity 73.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/041,075A
CURRENT FILING DATE: 1998-03-10
FRIOR APPLICATION NUMBER: 60/043,591
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                  GENERAL
                                                                                                                                                                              Sequence 30, Application US/09595684B Patent No. 6544766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: CDS
LOCATION: (300)..(1739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Candida kruisii
TITLE OF INVENTION: Human kinesins and methods of producing TITLE OF INVENTION: and purifying human kinesins FILE REFERENCE: cytop036 CURRENT APPLICATION NUMBER: US/09/595,684B
                                                                                                 APPLICANT: Beraud, Christophe
APPLICANT: Ohashi, Cara
APPLICANT: Sakowicz, Roman
APPLICANT: VAisberg, Eugeni
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Candida kruisii
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Local Similarity 100.0%; F
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                                                                                                                                                                                                                                                                                     1560 GAUGAUUCUGAUGACGACC 1578
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                                                                                                                                                                    INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Ver.
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                                                                   Sakowicz, Roman
VAisberg, Eugeni
Wood, Kenneth
Yu, Ming
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L00.0%; Pred. No.
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; Pred. No. 25;
5; Mismatches
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25;
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CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 8257
TYPE: DNA
ORGANISM: Human
                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (91)..(8082)
US-09-620-312D-130
                                                                                                                                                                                                                                                                              APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION UMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
CORTMANDE. of FI. GRAMES VETRION 1.0
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US-09-620-312D-130
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SEQ ID NO 130
LENGTH: 8503
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                                                                                  Query Match 0.6%; Score 19; Best Local Similarity 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 130, Application US/09620312D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2141
2141 TTGATCTGGAGAAAGAATT 2159
                                2873 TTGATCTGGAGAAAGAATT 2891
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Wang, Zhiwei
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                                                                   Conservative
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25;
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Search completed: April Job time: 165.43 secs

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RESULT 15 US-09-163-748C-3/c

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                                                                     Query Match
Best Local Similarity
Matches 19; Conserv
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CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09163748C Patent No. 6509172
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DeBacker, Oliver
APPLICANT: Van den Eynde, Benoit
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode Member
TITLE OF INVENTION: Family, The Proteins Encoded, And Uses Thereof
FILE REFERENCE: LUD 5558
                                                                                                                                                                               LENGTH: 9531
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: unsure
LOCATION: 92,232,1041,7412,9038-9040
OTHER INFORMATION: identity of several nucleotides not known
7045 TACAAAATGAAAACAAA 7027
                                  91 ТАСААЛАТGАЛЛАСАЛЛА 109
                                                                              Conservative
                                                                       0.6%; Score 19; DB
100.0%; Pred. No. 25
tive 0; Mismatches
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seq length: 2000000000
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Gapop 60.0 , Gapext 60.0
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13304.392 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpna/US06
3: /cgn2_6/ptodata/2/pubpna/US06
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4 2 2 1	22 21 21	0.6	6136 9888 2164 6048	16 14 15	US-10-257-166- US-10-311-455- US-10-027-632- US-10-311-455-
	4 N	21 21	0.6	6048 6072	14 14	US-10-311-455-4 US-10-311-455-4
	7 6	21	, o	8245 476	12	US-10-221-714A-170
ი	89	20	0.6	654	φ	US-09-736-734-1
O	9	20	0.6	654	14	US-10-396-911-1
	10	20	0.6	1023	14	US-10-074-475-133
	11	20	0.6	1377	12	US-10-424-599-91177
ი	12	20	0.6	1461	12	US-10-282-122A-10949
	13	20	0.6	1589	12	US-10-424-599-91176
	14		0.6	2418	15	US-10-108-260A-1756
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RESULT 2

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14	15	12	14	14	12	14	12	9		14	14	14	14	14	12	14	16	14	14	14	14	14	12	14	14	12	14	14	12
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Sequence 1881, Ap	19246,	92	2	e	8	Sequence 2098, Ap	Sequence 502, App	ŗ		w	_			æ	Sequence 499, App	æ		191,	39,	e 291,	e 2085,	1883,	35	7,	Ø	e 376	e 212:	Sequence 796, App	Sequence 98, Appl

ALIGNMENTS

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                                                               Query Match
Best Local Similarity
Watches 22; Conserva
                                                                                                                                                                        SEQ ID NO 123
; LENGTH: 6136
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-123
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Sequence 123, Application US/10257166
Publication No. US20040023230A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of TITLE OF INVENTION: Genes Implicated in Pharmacogenomics FILE REFERENCE: 5013.1011 CURRENT APPLICATION NUMBER: US/10/257,166 CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: PCT/EP01/07470
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                             2000-09-01
NUMBER OF SEQ ID NOS: 178
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                                                                                                                                                                                                                                                                                                                                                                                                                        DE 10032529.7
DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                2000-06-30
                       3145 TATTTTGTTTTTTTTTGGTAAA 3166
2122 TATTTTTTTTTTTTGGTAAA 2143
                                                                                 0.7%; Score 22; DB 16; Length 6136; ilarity 100.0%; Pred. No. 3.6; Conservative 0; Mismatches 0; Indels
                                                                                    0,
                                                                                    Gaps
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US-10-311-455-1214
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1214
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION UNMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1214
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LENGTH: 2164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 250839, Application US/10027632
Publication No. US20030204075A9
  Query Match
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
                                                                                            ORGANISM: Human
-10-027-632-250839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                     FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
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FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
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0.6%; Score 21; DB 15; ilarity 100.0%; Pred. No. 11; Conservative 0; Mismatches 0
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100.0%; Pr
1.72 0;
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RESULT 4
US-10-311-455-482
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                                                                             , OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: OLEK, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 482
LENGTH: 6048
                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 4
LENGTH: 6072
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Query Match
Best Local Similarity
Matches 21; Conserv
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System |
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
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                                                                                                                                                                                                                                           APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ)
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION CYTOSINE methylation
TITLE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
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                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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o. US20030143606A1
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                 0.6%; Score 21; DB 14; Length 6072; 100.0%; Pred. No. 12;
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100.0%; Pred. No.
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US-10-221-714A-170

3717 TATTTTGTTTTTTTTGGTAA 3737

TATTTTGTTTTTTTTGGTAA 3165

Publication No.

Application US/10221714A

US20040048254A1

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; OTHER INFORMATION: US-10-221-714A-170
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Sequence 87, Application US/10001843
Publication No. US20020132255A1
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Best Local Similarity
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SEQ ID NO 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                 FILE REFERENCE: DEX-0267

CURRENT APPLICATION NUMBER: US/10/001,843

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/249,992

PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Diagnosis of Diseases Associated with TITLE OF INVENTION: tumor suppressor genes and oncogenes FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: DE 10043826.1 PRIOR FILING DATE: 2000-09-01
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PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: DE 10013847.0
                                                                                                                                      APPLICANT: Turner, Leah
                                                                                                                                                                                            APPLICANT:
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OFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Cafferkey, Robert
Sun, Yongming
Liu, Chenghua
                      SEQ ID NOS: 218
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Query Match

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Score 20; DB 14;

Length 654;

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SEQ ID NO 1
LENGTH: 654
TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ROMEO, TONY
APPLICANT: ROMEO, TONY
TITLE OF INVENTION: ESCHERICHIA COLI CSRB
TITLE OF INVENTION: THEREBY, AND METHODS
FILE REFERENCE: 316082002001
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LENGTH: 476
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Best Local :
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CURRENT FELLOR DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/112,584
PRIOR APPLICATION NUMBER: 09/112,584
PRIOR APPLICATION NUMBER: 60/052,372
PRIOR PILING DATE: 1998-07-09
PRIOR PILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 10
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Patent No. US20020015983A1
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/396,911
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US/09/736,734
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/112,584
PRIOR FILING DATE: 1998-07-09
                                                                                                                   PRIOR APPLICATION NUMBER: 60/052,372 PRIOR FILING DATE: 1997-07-11
                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapien
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100.0%; Pred. No.
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Pred. No.
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32;
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US-10-074-475-133
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                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53343C.1 US-10-424-599-91177
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                                                                                                                                                                        APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
ITTLE OF INVENTION: Soy nucleic Acid Molecules and Other Molecules Associated With
ITTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
ITLE REFERENCE: 38-21(53223)B
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 91177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
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CURRENT FILING DATE: 2002-02-13
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EQ ID NO 133
LENGTH: 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/268,292 PRIOR FILING DATE: 2001-02-13
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                        Query Match 0.6%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 35; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                  ORGANISM: Glycine max
                                                                                                                                                               ENGTH: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E OF INVENTION: Compositions and Methods Relating to Breast Specific OF INVENTION: Genes and Proteins
REFERENCE: DEX-0313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3164 ААААТТТСАТАТБАААСТТА 3183
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1368 CAGTGGCATTGTCCAGCTTG 1387
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Hu, Ping
Herve
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Cafferkey, Robert
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5. US20030092898A1
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Conservative (
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Conservative 0;
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pred. No.
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                                                DB 12; Length 1377; 35;
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US-10-282-122A-10949/c
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US-10-424-599-91176
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                                                                                          GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 10949
LENGTH: 1461
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Chery
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blication No. US20040029129A1
                                                                                                                                   Sequence 91176, Application US/10424599 Publication No. US20040031072A1
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-02-16
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                  APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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20; Conserva
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Zyskind, Judith
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Yamamoto, Robert
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100.0%; Pred. No.
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TITLE OF INVENTION:

Plants and Uses Thereof for Plant Improvement

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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 1756
LENGTH: 2418
TYPE: DNA
ORGANISM: Homo sapiens
US-10-108-260A-1756
                                                          Sequence 1, Application US/09947953

Patent No. US20020155101A1

GENERAL INFORMATION:
APPLICANT: DONAHUE, J. KEVIN
APPLICANT: MARBAN, EDUARDO
TITLE OF INVENTION: CARGIAC
FILE REFERENCE: 71699/56415

FILE REFERENCE: 71699/56415

CURRENT APPLICATION NUMBER: US/09/947,953

CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/230,311
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/25,889
PRIOR FILING DATE: 2001-06-05

NUMBER OF SEO ID NOS: 2
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
LENGTH: 2985
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-947-953-1/c
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US-10-108-260A-1756
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US-10-424-599-91176
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 91176
LENGTH: 1589
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Publication No. US20040005560A1
GENERAL INFORMATION:
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Query Match
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ORGANISM: Glycine max
FEATURE:
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0.6%; Score 20; DB 9;
Length 2985;
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Beclin, C., Elmayan, T. and Vaucheret, H. Novel sgs3 plant gene and use thereof

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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DESCRIPTION OF THE PROTECTION	JOURNAL Patent: WO 0105951-A 2 25-JAN-2001; AVENTIS CROPSCIENCE S.A. (FR); INSTITUT NATIONAL DE LA RECHERCHE AVENTIS CROPSCIENCE S.A. (FR); INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (FR) Location/Qualifiers 1. 10878 /mol type="unassigned DNA" /db_xref="taxon:3702" 1. 10878 /note="unnamed protein product" /codon_start=1 /protein_id="CAC32419.1" /db_xref="REWTREMEL:CAC32419" /db_xref="R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The RIXEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Seker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M. Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., C.Heuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Open Reading Frame (ORF) Clones Unpublished
                                                                                                                                                                                                                                                                                                           The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Chan, M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,
                                                                                                                                                                               Yamada, K. (SSP/PGEC) and Seki, M. (F
to this work. Shinozaki, K. (RIKEN
/PGEC) contributed equally to this
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                          CTTGCAAGTGATTATGACTCGGATGTGAGTCAAAAGAGCCATGGATCACGAAAGCAG
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     CTTGCAAGTGATGATTATGACTCGGATGTGAGTCAAAAGAGCCATGGATCACGAAAGCAG
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1 (bases 1 to 2162)

1 (bases 1 to 2162)

1 yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Yu, G., Yuan, S., Carninci, P., Chen, H., Kawai, J., Xim, C.J., Narusaka, M., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Xim, C.J., Narusaka, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J. R. and Theologis, A.

Rocker, J. R. and Theologis, A.

Arabidopsis Full Length CDNA Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BT002944 2162 bp mRNA linear PLN 15-JAN-200 Arabidopsis thaliana clone RAFL14-93-K05 (R20243) unknown protein (At5g23570) mRNA, complete cds.
BT002944 BT002944.1 GI:27754622
                                                                                                                                                                        Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Direct Submission
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Street, Albany, CA 94710, USA
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'); Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shimn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A. d equally to (SSP/PGEC)

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (contributed equally to this work as PIs. Annotation based on July 2002 version of the Arabidopsis genome

FEATURES

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                                                                                                AACTTTGTGGCACCCCACCTGTATCTCGCCCCTCCTTTGGAAGGAGGATGGAATTGGCAG
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/note="This are a BamHI/KhoI insert.
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Mourrain, P., Beclin, C., Elmayan, T., Feuerbach, F., Godon, C., Morel, J.B., Jouette, D., Lacombe, A.M., Nikic, S., Picault, N., Remoue, K., Sanial, M., Vo, T.A. and Vaucheret, H. Arabidopsis SGS2 and SGS3 genes are required for posttranscriptional gene silencing and natural virus resistance Cell 10 (5), 533-542 (2000)
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Arabidopsis thaliana SGS3 gene,
AF239719
AF239719.1 GI:8164029
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Saint-Cyr, Versailles 78026, France
Location/Qualifiers
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VDNASEBENDSDALDDSDDLASDDYDSDVSQKSHGSRKQNKFKKFFGSLDSLSIBQ
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DKYEALLARHSYGPQHRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGQKRSM
FSGGVRQLYGFLATKQDLDIFNQHSQGKTRLKFELKSYQEMVVKELRQISEDNQQLNY
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/product="SGS3"
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Eucaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
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Submitted (02-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
On Sep 15, 2000 this sequence version replaced gi:4589439.
Address for correspondence: kaos@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd graph.cgi?c=MQM1 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/),
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Structural analysis of Arabidopsis thaliana chromosome 5. X.
Sequence features of the regions of 3,076,755 bp covered by sixty
Pl and TAC clones
DNA Res. 7 (1), 31-63 (2000)
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Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi). http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi). http://gene encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan-SE/). http://genome.wwstl.edu/eddy/tRNAscan
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QPLDDRNRKGKERAFGKYRYDLTVLLDVHTLLFSADCFSVFFFFMWFAIFICYFLISGG
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chromosome="5"
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KQHSDKAREDWLAAEKLNAEAAKKIIGITNKDNDIWKLDLHGLHATEAVQALQERDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="gene_id:MQM1.22
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(8642. .8705,8794. .8863,8978. .9387, 9584. .10347))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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                                                                                                                                                                                                                                                                    complement(12417. .13424)
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IGKHSRGQASLPLAVKTFFEDNRYRFDETRPGVITVRPKFRHS"
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                                                                                                                                                        id:MQM1.21"
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KQLVGAPLVSPDRTDWCWKAMGLNRDHEAVNVGGPNAVDISGLDYPSTMVVVAGFDPL
KQMQRSYYEWLKLCGKKATLIEYPNWFHAFYIFPELPEAGQLIMRIKDFVDERVASLS
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17943. 118110,18199. 118390)
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complement(join(18965..19043,19240..19298,19419.
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ragvpmevmglmlgbevdeytmrvudvfamfogstedvsveavudputpgytmmldmlkQtg
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rpemvvgwyhshegfgcwlsgvdintgosfealloravavvudpigsvgktviddar
sindotimlogerottskinlghlnkpsiqallhglnrhyysiainvekoeleekolle
lhkkkmtdgltlrrfdthsktineottoemlslaakknnkavqbedelspeklaivnvgr
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28385. .28604,28688. .28855,28944. .29092)
/note="gb]AAC97420.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similar to unknown protein"
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id:MQM1.16
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strong similarity to

unknown protein"

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TATAACCTGCACCCTCTACTAGCTCATGCGAGGACAAAAGGAGCTAGGCGAGTTAAGCTC
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                                                                              GAACCACAGAGGCAGTGGCATTGTCCAGCTTGTCAGAACGGACCTGGTGCCATCGATTGG
                                                                                                        GAACCACAGAGGCAGTGGCATTGTCCAGCTTGTCAGAACGGACCTGGTGCCATCGATTGG
                                                                                                                                                                             CTTGCAAGTGATGATTATGACTCGGATGTGAGTCAAAAGAGCCATGGATCACGAAAGCAG
                                                                                                                                                                                                                                                                                                            CTTGCAAGTGATGATTATGACTCGGATGTGAGTCAAAAGAGCCATGGATCACGAAAGCAG
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SIYSLAYERHKSWYSWILSSLTSCVYNFGFTMMCPQLFTNYKLKSVAHLDWRQMTYKF
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30341. .30493,30579. .30722,30956. .31484))
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100.0%; Pr
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Query Match Best Local Similarity Matches 289; Conserv

12.7%; ilarity 99.7%; Conservative

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Score 239; DB 8; Pred. No. 9.9e-131; 0; Mismatches 1;

Length 650;

Indels

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Gaps

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ACCESSION
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SOURCE
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TITLE
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MEDLINE
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                                                             misc_feature
                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brunaud, V., Balzergue, S., Dubreucg, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T_DNA integration into the Arabidopsis genome depends on sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunaud, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         left border; T-DNA flanking sequence Arabidopsis thaliana (thale cress)
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Direct Submission
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                    /note="T-DNA
left border"
                                                             /clone_lib="Arabidopsis thaliana
1. .650
                                                                                                         /clone="157C08"
                                                                                                                                                  /mol_type="genomic DNA"
/cultivar="Wassillewskija"
                                                                                                                                                                                              organism="Arabidopsis thaliana"
                                                                                                                              /db_xref="taxon:3702"
                                         flanking sequence
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RES Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Barnstead, M., Benahmed, F., Baldhin, D., Badaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldhin, D., Badar, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blarch, P., Burrell, K., Calderon, E., Chu, J., Chacke, J., Cokrell, R., Cox, C., Coyle, M., Cree, A., D. Souza, L., Clackeo, J., Chen, R., Chen, Y., Chen, Z., Chu, J., Chackeo, J., Chen, R., Chen, Y., Chen, Z., Chu, J., Checkeo, J., Coxerell, R., Cox, C., Coyle, M., Cree, A., D. Souza, L., Cleveland, C., Davis, M., Cree, A., D. Souza, L., Cleveland, C., Davyla, M., Cree, A., D. Souza, L., Coxerell, R., Coxerell, R., Coxerell, D., Dayal, R., Chen, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Delgado, O., Denson, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Dayal, R., Chen, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Drager, H., Dayan-Rocha, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Drager, H., Dayan-Rocha, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Drager, H., Dayan-Rocha, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Drager, H., Dayan-Rocha, S., Chen, S., Chan, M., Garcia, M., Garcia, M., Garrer, T., Garza, M., Fraser, C.M., Falls, T., Fan, G., Chen, R., Chan, M., Garcia, M., Garrer, T., Garza, M., Gebregeor, G., Hamilton, K., Galder, M., Garrera, M., Gester, M., Harley, M., Harley, M., Harley, M., Harley, M., Harley, M., Harley, M., Handlon, M., Hamilton, K., Hogues, M., Hogues, M., Hogues, M., Hodyson, A., Hogues, M., Guevara, W., Garcia, M., Harley, S., Kaly, S., Kaly, S., Khan, Z., King, L., Li, Z., Liu, J., Kowar, S., Kaly, S., Man, Z., Kose, M., Marlin, R., Li, Z., Liu, J., Kovar, 
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Mammalia; Eutheria; Rodentia;
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IN PROGRESS
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FEATURES

organism="Rattus norvegicus"/

Location/Qualifiers

175437 175537 176580

175436: contig of 175436 bp in length 175536: gap of unknown length 176579: contig of 1043 bp in length 176679: gap of unknown length 178928: contig of 2249 bp in length.

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Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Strand, G., Strong, R., Sutton, A., Svatek, A., Trejos, Z., Usmani, K., Taylor, T., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, I., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Willson, R., Miczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., yon, V., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
On Oct 11, 2002 this sequence version replaced gi:21909375.
On Oct 11, 2002 this sequence version replaced gi:21909375.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.ttmc.edu/projects/rat/). Each contig described (http://www.hgsc.bcm.ttmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas in the feature contig-scaffold). Within each contig-scaffold, assembly (a 'contig-scaffold'). Within each contig-caffold, and separated individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is is not known and their order in this sequence record as arbitrary. Gaps between the contigs are represented as arbitrary. He exact sizes of the gaps are unknown. This record will be updated with the finished sequence This record will be updated with the sinished sequence as it is available and the accession number will be second as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
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VERSION
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AL928719/c
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                                                                                                         Submitted (28-JAN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 3, 2002 this sequence version replaced gi:24395353. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL928719 197909 bp DNA li
Mouse DNA sequence from clone RP23-419G21 on
During sequence assembly data is compared from overlapping clones.
                                    Contact: humquery@sanger.ac.uk
                                                         Web site:
                                                                         Center: Wellcome Trust
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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clone_end:T7
site:MboI
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/note="wgs_end_extension
clone_end:Sp6"_
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clone_end:T7"
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173824. .175436
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complement(172023.
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clone_end:Sp6"
27453. .29430
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156410. .157915
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/note="wgs_end_extension
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                                                       http://www.sanger.ac.uk
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/db_xref="taxon:10116"
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100.0%; Pred. No. 2.1;
tive 0; Mismatches
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-419G21 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 214186)

Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Dietrich, N.L., Eagle, W.O., Gupta, J., Ho, S.-L., Huang, M.C., Idol, J., Lee-Lin, S.-Q., Maduro, Q.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Ojodu, M.A., Pearson, R., Stantripop, S., Summers, T.J., Thomas, J.W., Thomas, P.J., Tiongson, E., Touchman, J.W., Tran, J.T., Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC078933 214186 bp DNA linear HTG 11-J
Mus musculus chromosome 5 clone RP23-201E13 strain C57BL6/J
WORKING DRAFT SEQUENCE, 17 unordered pieces.
                                                                                                                                  Submitted (11-AUG-2000) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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AC078933.1 GI:9795569
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                        Green, E.D.
                                                                                                                                                                                                                                                                                                       NISC Mouse Sequencing Initiative
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                                                                                                                                                                                                                                                     (bases 1 to 214186)
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                      Center code: NISC
                                                                                 Center: NIH Intramural Sequencing Center
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mol_type="genomic DNA"
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                                                                                                                Genome Center
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Assembly program: Phrap; version 0.990319
Consensus quality: 207891 bases at least Q40
Consensus quality: 207891 bases at least Q30
Consensus quality: 209797 bases at least Q20
Insert size: 118000; agarose-fp
Insert size: 218000; pulse-field-gel
Insert size: 217000; pulse-field-gel
Quality coverage: 4.43x in Q20 bases; agarose-fp
Quality coverage: 4.43x in Q20 bases; pulse-field-gel
Quality coverage: 4.94x in Q20 bases; sum-of-contigs
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153409
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                    7723. .13087
                                                                             3308. .7622
                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL6/J"
                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                    db_xref="taxon:10090"
chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     52196: gap of unknown length
62100: contig of 95114 bp in length
62200: gap of unknown length
77345: contig of 15145 bp in length
77445: gap of unknown length
87428: contig of 983 bp in length
100606: contig of 13078 bp in length
100706: gap of unknown length
117904: contig of 17198 bp in length
118004: gap of unknown length
118014: gap of unknown length
118015: gap of unknown length
135715: contig of 17711 bp in length
135815: gap of unknown length
153408: contig of 17593 bp in length
153408: contig of 17595 bp in length
181134: gap of unknown length
181136: contig of 33052 bp in length
                                                                                                     'note="assembly_fragment"
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                                        note="assembly_fragment"
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3307: gap of unknown length
7622: contig of 4315 bp in length
                                                                                                                                                                           lib="RPCI mouse BAC library 23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACO79182 218774 bp DNA linear HTG 23-AUG-2000
Mus musculus chromosome 5 clone RP23-203F6 strain C57BL6/J, WORKING
DRAFT SEQUENCE, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC079182.1 GI:9886001
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
                                                                                                               Direct Submission
Submitted (23-AUG-2000) NIH Intramural Sequencing
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                             Green, E.
                                                                                                                                                                                                                                                                                                    NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                        (bases 1 to 218774)
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                    Center: NIH Intramural Sequencing Center Center code: NISC
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100707. .117904
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135816. .153408
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181135. .214186
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153509. .181034
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Gaps

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NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: ve
Center clone name: 203F06
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Contact: nisc_mouse@nhgri.nih.gov
------- Project Information
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                            /note="assembly_fragment"
4971. .8469
                                                                 2102. .4870
       /note="assembly_fragment"
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                                                                                                                       clone_
                                                                                                                                                            /db_xref="taxon:10090"
/chromosome="5"
                                                                                                                                                                                             'mol_type="genomic DNA"
'strain="C57BL6/J"
                                                                                                                                                                                                                                                                      ocation
                                                                                                                                         clone="RP23-203F6"
                                                                                                                                                                                                                                 organism="Mus musculus"
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g of 28172 bp in
of unknown length
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1 g of 14504 bp in )

1 mown length
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of 8381
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of 3499
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; pulse-field-gel
; sum-of-contigs
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RS Muzny, D. Marie . Metsker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Barber, M., Baca, E., Baden, H., Baddwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Durnha, D., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hadlun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
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HTG; PHASE1; HTGS DRAFT; HTGS FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC115306 236508 bp I
Rattus norvegicus clone CH230-11F1,
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21732. .29661
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184946. .218774
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|53457. .184845
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HTG 23-NOV-2002

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FEATURES

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Jackson, L., Jacob, L., Jiang, H., Johnson, R., Johnson, R., Zoliver, A., Kargethy, S., Keily, S., Keily, S., Kaily, S., Kaily, S., Kaily, S., Kaily, S., Kaily, S., Kay, L., Li, Z., Liu, J., L
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TITLE
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COMMENT

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FEATURES
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AC140364
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         280016 bp DNA linear H Mus musculus chromosome UNK clone RP24-75K5, WORKING SEQUENCE, 8 unordered pieces.
AC140364
AC140364.2 GI:38176012
HTG; HTGS PHASE1; HTGS PLAIT; HTGS_FULLTOP.
Mus musculus (house momos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity 100.0%; P
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                                                                                                                                                                                                                                                                   2 (bases 1 to 280016)
McPherson, J.D. and Wat
Direct Submission
                                                                                                                                                                                                                                                                                                                        wilson, R.K.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 280016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Center: Washington University Genome (center code: NUGSC web site:http://genome.wustl.edu Contact: submissions@watson.wustl.edu Contact: Project Information ---
                                                                                                                        Submitted (05-NOV-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On NOV 5, 2003 this sequence version replaced g1:28475622.
                                                                                                                                                                                                                 Parkway, St. Louis, MO
3 (bases 1 to 280016)
                                                                                                                                                                                                                                    Submitted (23-FEB-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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125419
180276
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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235232. .236508
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233371. .235181
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125418: gap of unknown length
180275: contig of 54857 bp in length
180375: gap of unknown length
236508: contig of 56133 bp in length
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                                                                                              Genome Center -----
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                        567 TGTGAGTCAAAAGAGCCATGGA 588
  AC073813 304407 bp DNA linear HTG 29-JUN-2000 Mus musculus clone RP23-69B1, WORKING DRAFT SEQUENCE, 58 unordered
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Sequencing vector: Dlasmid; 1008
Chemistry: Dye-primer ET; 08 of reads
Chemistry: Dye-terminator Big Dye; 1008 of re
Chemistry: Dye-terminator Big Dye; 1008 of re
Chemistry: Dye-terminator Big Dye; 1008 of re
Chemistry: Dye-terminator Big Dye; 1008 of re
Chemistry: Dye-terminator Big Dye; 1008 of re
Chemistry: Dye-terminator Big Dye; 1008 of re
Chemistry: 278028 bases at least Q40
Consensus quality: 278087 bases at least Q30
Consensus quality: 279492 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available be preserved.
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198321. .280016
/note="assembly_name:Contig28"
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48534. .85803
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0500/ 137685
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303. .3866
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1302: gap of unknown length
3866: contig of 2564 bp in length
3866: gap of unknown length
24768: contig of 20802 bp in length
24868: gap of unknown length
48433: contig of 23555 bp in length
48533: gap of unknown length
48533: gap of unknown length
85803: contig of 37270 bp in length
85803: contig of 37270 bp in length
127685: contig of 41782 bp in length
127785: gap of unknown length
127785: gap of unknown length
198220: contig of 70435 bp in length
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                                                                                                                                                                                                       Score 22; DB 2;
Pred. No. 2.1;
0; Mismatches
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                                                                                                                                                                                                                                                Length 280016;
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AUTHORS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 257140 bases at least Q40
Consensus quality: 282847 bases at least Q30
Consensus quality: 288639 bases at least Q30
Consensus quality: 288639 bases at least Q20
Estimated insert size: 272860; agarose-fp estimation
Estimated insert size: 298707; sum-of-contigs estimation
Quality coverage: 9.46 in Q20 bases; agarose-fp estimation
Quality coverage: 8.64 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
consists of 58 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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AC073813
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Center clone name: RPCI-23_69B1
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC073813.1 GI:8810430
HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia;
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Ng, W. V., Kennedy, S. P., Mahairas, G. G., Berquist, B., Pan, M., Shukla, H.D., Lasky, S. R., Baliga, N., Thorsson, V., Sbrogna, J., Shukla, H.D., Lasky, S. R., Baliga, N., Thorsson, V., Sbrogna, J., Swartzell, S., Weir, D., Hall, J., Dahl, T. A., Welti, R., Goo, Y. A., Leithauser, B., Keller, K., Cruz, R., Danson, M. J., Hough, D. W., Leithauser, B., Keller, K., Cruz, R., Danson, M. J., Hough, D. W., Maddocks, D. G., Jablonnik, P. E., Krebs, M. P., Angevine, C. M., Dale, H., Isenbarger, T. A., Peck, R. F., Pohlschrod, M., Spudich, J. L., Jung, K. -H., Alam, M., Freitas, T., Hou, S., Daniels, C. J., Dennis, P. P., Jung, K. -H., Alam, M., Freitas, T., Hou, S., Daniels, C. J., Hood, L. and Omer, A. D., Ebhardt, H., Lowe, T. M., Liang, P., Riley, M., Hood, L. and
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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Submitted (14-JUL-2000) Institute for Submitted Way NE, Seattle, WA 98105, (Roosevelt Way NE, Qualifiers
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ILRRIERDVVERGRELEGVMDQYLSTVKPMHEQFIEPTKRHADIIIPEGANSVAVNLL
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ABL15067

New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene expression.

The present sequence encodes the Arabidopsis thaliana SGS3 polypeptide The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of

Claim 1; Page 32-35; 36pp; French.

(AVET)

AVENTIS CROPSCIENCE SA.
INST NAT RECH AGRONOMIQUE.

16-JUL-1999; 99FR-00009417. 26-JAN-2000; 2000FR-00001006. 13-JUL-2000; 2000WO-FR002052 25-JAN-2001.

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WPI; 2001-159529/16. P-PSDB; AAB31798.

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ALIGNMENTS

RESULT 1 AAF25374 ID AAF2 XX AAF2 XX AAF2 XX AAF2 XX AAF2 XX AAF2 XX XX VI XX VI XX VI FT CD FT SGS3 gene; post-transcriptional inactivation; RNA degradation; viral resistance; resistance; fatty acid content; protein content; Nucleotide sequence of the Arabidopsis SGS3 polypeptide. WO200105951-A2. Arabidopsis thaliana. 15-MAY-2001 AAF25374; AAF25374 standard; cDNA; 1878 (first Location/Qualifiers 1. .1878 /product= "SGS3" entry) ВP

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RESULT 2 AAF25373 ID AAF25373 standard; DNA; 3275 BP.

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Query Match
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                                                                                                                                                                       The present sequence represents the genomic sequence of the Arabidopsis thaliana SGS3 gene. The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased resistance to viruses, while inactivation of SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous recombination) increases the level of the transgene product. This product may e.g. impart resistance (to herbicide, insects or pathogens), alter contents cessential fatty acids or proteins, or is pharmaceutically active, e.g. is
                                                                                                                           Sequence 3275 BP;
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1 ATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAGAACGTTCAGGGTGGTTATAGGCCT
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26-JAN-2000; 2000FR-00001006.
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26-JAN-2000; 2000FR-00001006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUL-2000; 2000WO-FR002052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-159529/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New SGS3 gene from Arabidopsis
resistance in plants and, when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23
                                                                                                                                                                                                                    Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; expressed sequence trag; Fusarium venenatum; Aspergillus niger; Aspergillus oryvae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; culture condition; environmental stress; spore morphogenesis; ss. metabolic pathway engineering; catabolic pathway engineering;
                                                                                                                                                                                                                                                                                                                                                                                  AAF12773 standard; cDNA; 596 BP
                                                                                                                                                                                                                                                                                                    Aspergillus oryzae EST SEQ ID NO:5296.
                                                                                                                                                                                                                                                                                                                                13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                          AAF12773;
                                                                                                               22-MAR-2000; 2000WO-US007781
                                                                                                                                            28-SEP-2000
                                                                                                                                                                       WO200056762-A2.
                                                                                                                                                                                               Aspergillus oryzae.
                                                                                          22-MAR-1999;
WPI; 2000-594572/56
                         Berka RM,
                                                 (NOVO ) NOVO NORDISK BIOTECH INC.
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INST NAT RECH AGRONOMIQUE.
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                          Rey MW,
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                                                                                           99US-00273623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                              Shuster JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaucheret H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20;
Pred. No.
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n inhibited,
                                Kauppinen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amplify cDNA encoding an Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for increasing virus, for increasing transgene
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                                    Clausen IG,
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RESULT 6
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AC AAH93017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC cells. The method uses fluorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring the CC global expression of genes from FF cells allows the production potential CC of the microorganisms to be improved. New genes may be discovered, CC possible functions of unknown open reading frames can be identified and CC genes can be used to study how FF cells addapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, CC metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of candidancy as one spot on an array equals one gene or open reading frame, CC and organisation of the microarrays based on function of the gene copy for facilitate analysis of the results. AAF11248 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents CC Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from CC Trichoderma reesei, which are all specifically claimed in the present
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human inflammatory bowel disease related gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags.
                                                                                                                                                                                                                                                                                        11-DEC-2000; 2000WO-US033632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 TCCAAGAAGAACAAGAACAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88; Page 2210; 3161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             esent invention describes a method for monitoring differential sion of genes in a first filamentous fungal (FF) cell relative is sion of the same genes in one or more second filamentous fungal The method uses fluorescence-labeled nucleic acids isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                    WHITEHEAD INST BIOMEDICAL RES. ELLIPSIS BIOTHERAPEUTICS CORP.
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                                                                                                                                                                                              99US-0170257P.
2000US-0196046P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphism; SNP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  forensic test; gene therapy; ds.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 19p13;
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58;
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Lander ES,

Rioux J,

Siminovitch

AAA81304 to AAA81321 represent PCR primers

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AAA81465/c
II AAA814
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a gene containing a polymorphic site described in the exemplification of the
            The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and
                                                                                                                                                                                                                               Frazer CM, Hickey E,
Masignani V, Galeotti
Rappuoli R, Pizza M;
                                                                                                        Claim 7; Page 383-397; 1760pp; English.
                                                                                                                                      Neisserial infections,
                                                                                                                                                     Isolated nucleotide sequences of Neisseria meningitidis which in the diagnosis and treatment of N. meningitidis infection an
                                                                                                                                                                                                   WPI; 2000-318079/27.
                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200022430-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis; Neisseria gonorrheae; genome; antigen; vaccine; diagnosis; infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N. meningitidis partial DNA sequence gnm_13 SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay.
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                                                                                                                                                                                                                                                                                             (CHIR ) CHIRON
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                               CORP.
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99US-0132068P
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                                                                                                                                     for example, N.gonorrhoea.
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Mismatches
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                                                                                                                                                                                                                                               Tettelin H, Venter
Ratti G, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogenic;
; identification;
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                                                                                                                                                                                                                                                  Scarlato
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                                                                                                                                                                     can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
AAA81489 5/c
AAA81489 5/c
Continuation (6 of 9) of AAA81489 from base 500001 (N. meningitidis partial DNA sequence Continuation (6 of 9) of ragments LOCUS AAA81489 Accession Aaa81489
WP Sequence split into 9 fragments LOCUS AAA81489 Accession Aaa81489
WP Fragment Name Begin 10000
WP FAAB1489 100001 210000
WP AAA81489 100001 210000
WP AAA81489 300001 410000
WP AAA81489 400001 510000
WP AAA81489 500001 510000
WP AAA81489 500001 510000
WP AAA81489 500001 710000
WP AAA81489 600001 710000
WP AAA81489 700001 810000
WP AAA81489 800001 837096
RESULT 9
ABQ88198/c
ID ABQ881
XX ABQ881
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XX ABQ881
XX OATHOR
DT 18-SEP
XX Human;
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XX Homo i
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XX PD 27-JU
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variable regions
                                                                                                                                                        Human; osteoblast; stem cell differentiation; bone tissue deposition,
                                                                                                                                                                                                Human osteoblast differentiation related cDNA SEQ ID NO 105.
                                                                                                                                                                                                                                                                                                                   ABQ88198 standard; cDNA; 154902
                                                                                                                                                                                                                                          18-SEP-2002
                                                                                                                                          osteoporosis;
                                                              WO200250301-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23354 GAACAGTTGGTTCAAGGTTT 23335
                                                                                                                                                                                                                                                                                                                                                                                                                     32595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 GAACAGTTGGTTCAAGGTTT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                        67 GAACAGTTGGTTCAAGGTTT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   ĠAAĊAĠŢŢĠĠŢŢĊAAĠĠŢŢŢ 32576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                            osteopathic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 3; pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 47475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110000;
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27-JUN-2002

30-APR-1999; 08-OCT-1999;

99US-0132068P. 99WO-US023573.

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The invention relates to genes and their expression profiles are used for: (a) screening modulators of precursor stem cell differentiation into consteoblasts, or bone tissue deposition; (b) diagnosing abnormal consteoblasts, or collection of bone tissue, abnormal rate of osteoblast formation or cited in (b), or monitoring the progression of bone tissue deposition. Conted in (c), or monitoring the progression of bone tissue deposition. Consteoblast or male osteoporosis, osteoporosis, glucocorticoid consteoporosis or male osteoporosis, osteoporia, osteopory, drugtinduced abnormalities in bone formation or bone loss, conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), conditions that continue altered bone metabolism (e.g. idiopathic juvenile osteoporosis), c
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XX OB-NAR
XX OB-AAR
PR 30-APR
PR 08-OCT
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Best Local S
Matches 20
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24-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 105; 78pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-557663/59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 154902 BP; 43917 A; 31458 C;
                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis B nucleotide sequence SEQ ID NO:113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF21612 standard;
                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                             AAF21612;
                                                                                                                                                                                                                                                                   diagnosis; antigen; detection; infection;
                                                                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
                                                                                                                                                                                                 Neisseria meningitidis
                                                                  08-MAR-2000; 2000WO-US005928.
                                                                                                                 09-NOV-2000
                                                                                                                                                         WO200066791-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1712 TGGAGGAGTTTTGTGGAAGAG 1731
|||||||||||||||||
128153 TGGAGGAGTTTGTGGAAGAG 128134
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PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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2001US-0285691P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                       entry)
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
54;
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                                                                                                                                                                                                                                                                             gene therapy; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 154902;
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RESULT 11
AAA68016/c
ID AAA680
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XX AAA680
XX Eucaly
XX Plant;
KW Pinus
XX Pinus
XX W02000
XX Eucaly
XX O9-OCT
PF 06-OCT
XX 09-OCT
PR 14-JUL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes the full length genome of Neisseria CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 CC represent fragments of the NMB genomic sequence, as the sequence was too CC long to go in a record on its own it was split into 8 sequences which CC overlap each other at the beginning and end of each sequence by 49980 bp CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of CC AAF21607, the last 49980 bp of AAF21589 encode the Neisseria proteins CC given in AAB58550 to AAB58533, and AAF21588 encode the Neisseria proteins CC primers which are used in the exemplification of the present invention. CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins CC and/or antibodies which binds to the proteins can be used in compositions CC for treating or preventing infection due to Neisserial bacteria or as a CC diagnostic reagent for detecting the presence of Neisserial bacteria or CC of antibodies raised to Neisserial bacteria. Computers, computer memory, CC computer storage medium or computer databases can be used in a search to CC identify open reading frames (ORFs) or coding sequences within the NMB CC genome. The DNA sequences provide further opportunities to find antigenic CC outer membrane proteins currently used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                   09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                   Plant; lignin; lignin bi
Pinus radiata; Monterey
                                                                                                                                                                                                                                                        Eucalyptus grandis CCR nucleotide sequence SEQ ID NO:109.
                                                                                                                                                                                                                                                                                                                            AAA68016;
                                                                                                                                                                                                                                                                                                                                                              AAA68016 standard; DNA; 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 349980 BP; 86473 A; 95646 C; 85908 G;
                                                                     06-OCT-1999;
                                                                                                                                       WO200022099-A1
                                                                                                                                                                     Eucalyptus grandis
                                                                                                                                                                                                                                                                                            24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis B full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pizza M, Hickey E, Peterson J,
Masignani V, Galeotti C, Mora M,
Rappuoli R, Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000GB-00004695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frames are used to detect, treat and
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INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACAGTTGGTTCAAGGTTT 167805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACAGTTGGTTCAAGGTTT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                        (first entry)
                 98US-00169789
99US-0143811P
                                                                                                                                                                                                                   lignin biosynthetic pathway; Eucalyptus grandis;
                                                                   99WO-NZ000168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; 5cc
100.0%; Pr
                                                                                                                                                                                                       pine;
                                                                                                                                                                                                                                                                                                                                                              ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20;
Pred. No.
                                                                                                                                                                                                          ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tettelin H,
, Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome sequence and open reading prevent Neisserial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 349980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81953 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                       S
                                                                                                                                                                            The present invention describes isolated polynucleotides and proteins CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), conmarate 3-hydroxylase (C3H), phenolase (PNL), 0-methyl transferase CC (CMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-coA reductase CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC claccase, peroxidase, ferulate-5-hydroxylase (FSH), alpha-amylase, caffeic CC acid methyl transferase, caffeoyl COA methyl transferase, coumerate COA (CC acid methyl transferase, caffeoyl COA methyl transferase, coumerate COA (CC acid methyl transferase, caffeoyl COA methyl transferase, coumerate COA (CC acid methyl transferase, caffeoyl COA methyl transferase, which are CC used for modulating lignin content, lignin composition and the structure CC of a plant, especially eucalyptus and pine species, and for modifying the CC activity of an enzyme involved in lignin biosynthetic pathway, and for corducing a plant having altered lignin content, composition and CC structure. They can be used for designing probes and primers useful for CC detecting similar DNA and RNA sequences in any organism and for PCR conjuncteotides. AAA67908 to AAA68201 and AAB16341 to AAB16449 represent CC polynucleotide and protein sequences used in the exemplification of the Cr present invention.
                                                                                  Query Match
Best Local S
Matches 19
                                                                                                                                                                          Sequence 481 BP; 122 A; 118 C; 111 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polyncleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and structure.
                                                                                                                                                                                                                        present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 91-92; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-317962/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                           74
                                                                                       19,
                                                                                                            Similarity
                           TGGTTCAAGGTTTGGCAGG
TGGTTCAAGGTTTGGCAGG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ę,
                                                                                  larity 100.0%; 1 Conservative 0;
                                                                                                                              1.0%;
                                                                                                       Score 19;
; Pred. No.
                                           92
                                                                                       Mismatches
                                                                                                                                                                          130 T; 0 U; 0 Other;
                                                                                                                                DB 3;
                                                                                     1.8e+02;
hes 0;
                                                                                                                              Length 481;
                                                                                       Indels
                                                                                     0,
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RESULT 12
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21-NOV-1997;
09-OCT-1998;
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lignin biosynthesis; gene.
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                                                        2000US-00615192
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99US-0143833P
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97US-00975316.
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ARK64246
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AC AAK64
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide associated with the lignin biosynthetic pathway, for modulating lignin content, composition and structure of plants, or producing a plant with altered lignin content, composition and structure.
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11-JUL-2000;
14-JUL-2000;
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04-FEB-2000;

24-FEB-2000;

02-MAR-2000;

16-MAR-2000;

17-MAR-2000;

19-MAY-2000;

19-MAY-2000;

07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:9306.
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19; Conserv
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HAVUKKALA I.
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2000US-0184664P.

2000US-0184663P.

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2000US-0199074P.

2000US-0199076P.

2000US-0199076P.

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2000US-0214866P.

2000US-021486P.

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1.8e+02;
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12-SEP-2000;
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2000US-0225213P.
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2000US-0237037P.
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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAW82170 to AAW91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting the CC nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic CC to AAK87694 represent human immune/haematopoietic antigen genomic
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
05-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
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the present invention. AAK54942

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antigen genomic AAK54950 and AAM82169

Query Match Best Local Similarity

100.0%; 1.0%;

Score 19; Pred. No.

DB 2; L

Length 495

Sequence 495

BP; 126 A; 121 C; 116 G; 132 T; 0 U; 0 Other;

cancers

polypeptides, and metastasis.

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ARESULT 14
AAV23847/c
ID AAV238
XX AAV238
XX Lignin
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                                                                                    This sequence represents a fragment of the CCR enzyme coding sequence. It CC is an example of a DNA sequence of the invention, which are from CC Eucalyptus grandis (eucalyptus) and prinus radiata (pine) associated with the lighin biosynthesis pathway. Constructs containing the DNA sequences CC can be used to produce transgenic plants or plant cells, especially woody plants e.g. eucalyptus or pine species but also e.g. monocotyledons or CC dicotyledons; by stably incorporating the constructs into the plant CC genome. The lighin content or structure, or activity of a specific enzyme in the plant, can therefore be modulated. Reductions in lighin content or CC changes in composition are useful in tree processing for paper. High lighin content results in energy- and chemical-intensive separation methods in order to obtain the pure cellulose fibre required. Reductions in lighin content may also be useful for forage crops, whilst increases in lighin content may also be useful for increase the mechanical strength of wood, change its colour or increase the mechanical corporate are also useful as probes to isolate DNA sequences encoding enzymes involved in the lighnin biosynthesis pathway from other plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences useful for modification of plant lignin content or structure from Eucalyptus grandis (eucalyptus) and Pinus radiata (pine) are associated with lignin biosynthesis pathway, useful e.g. in paper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 39; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-207374/18.
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                                                                                                                                                            This sequence represents a cinnamoyl-CoA reductase (CCR) partial CDNA CC from Eucalyptus grandis. This enzyme is involved in the biosynthesis of CC lignin, an insoluble polymer which is primarily responsible for the CC rigidity of plant stems. Lignin serves as a matrix around the CC polysaccharide components of some plant cell walls. The higher the lignin CC content, the more rigid the plant. Lignin also plays a role in disease CC resistance of plants by impeding the penetration and propagation of CC pathogenic agents. Lignin is formed by polymerisation of at least three CC pathogenic agents. Lignin is formed by polymerisation of at least three CC pathogenic agents of three monolignols are synthesised by similar CC sinapyl alcohol. These three monolignols are synthesised by similar CC pathways from phenylalanine in a multistep process and are believed to be CC plants can be altered using DNA sequences encoding these enzymes. CC Lignin content can be increased by incorporation of additional copies of genes encoding these enzymes into the target plant. This could be beneficial for increasing the mechanical strength of wood. Similarly, a decrease in lignin content can be obtained by transforming the target plant with antisense copies of such genes. This may be beneficial in CCC plants used as forage crops for livestock (lignin is indigestible) and in trees used in paper manufacture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated DNA sequence encoding enzymes from the lignin synthetic pathway useful for generating plants with an altered lignin content.
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			COMMENT	JOURNAL		TITLE		AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	RESULT 1 AQ959658/c	
For addtional information, see http://www.tigr.org/tdb/at/at.html	Tel: 301 838 0200 Fax: 301 838 0208	9712 Medical Center Dr., Rockville, MD 20850, USA	Contact: Xiaoying Lin	polymorphisms Unpublished (2000)	Arabidopsis thaliana and identification of sequence-based	Genomic survey sequencing of Landsberg erecta ecotype of	Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.	Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,	1 (bases 1 to 693)	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arabidopsis thaliana	Arabidopsis thaliana (thale cress)	GSS.	AQ959658.1 GI:6787359	AQ959658 Î	survey sequence.	FB LERE Arabidopsis thaliana genomic clone I	AQ959658 693 bp DNA linear GSS 28-JAN-2000		

Result No.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/clone lib="LERE"
/note="Organ: Leaf; Vector: pUC19UK; Total genomic DNA sheared to 0.6-0.8 Kbp before ligation."
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|mol_type="genomic DNA"
|strain="LANDSBERG ERECTA"
|db_xref="taxon:3702"
|clone="LEREM21"
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Pred. No. 1.6e-276;
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Query Match
Best Local Sim
Matches 534;
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1 (bases 1 to 606)

Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.

Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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For addtional information, see
Seq primer: TF
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Unpublished (2000)
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sheared to 0.6-0.8 Kbp
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/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
/clone="LEREM21"
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Pred. No. 1e-260;
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Kbp before ligation."
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Asamira, F., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV566465 Arabidopsis thaliana green thaliana cDNA clone SQ244b06F 3', mF AV566465 AV566465.1 GI:8737917 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Erika Asamizu
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                     ATGGAGGAGTTTGTGGAAGAGAGGGGAGATGCTGATAAAAGATCAAGAGAAGAAGAAGATGGAA
                                                                       GACGATTGCCGAAAGAGAGCTGAGGAAGTGTCAAGCTTCATCGAGTTTCAAGAGAAAGAG
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     ATGGAGGAGTTTGTGGAAGAGAGGGAGATGCTGATAAAAGATCAAGAGAAGAAGATGGAA
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asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone_Tib="Arabidopsis thaliana green siliques Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
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/mol_type="mRNA"
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/clone="SQ244b06F"
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                  512;
                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002)
Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
AU236368
AU236368.1 GI:19875537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4559
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakural,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AU236368 RAFL14 Arabidopsis 1
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                                                                                                                                                                                                                                                      GAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTTCACAAGATGAT 120
                                                                                                                                                                                                                                                                                                                            ATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAAGAACGTTCAGGGTGGTTATAGGCCT
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AGAGGTAGCAACGTATCTGGGAGAGGAAACAATGTATCCGGGAGAGGGTAACGGCAATGGT
                                                                          AAAACTTGGGTTTCTCAGAATTCGAAATCCTCCTAGAGCTTGGGGTGGTCAGCAGCAAGGG 240
                                                                                                                                                                                                                                 GAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTTCACAAGATGAT
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                                                                                                                                        GGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAAACACTTCTGGA
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                                               AAAACTTGGGTTTCTCAGAATTCGAATCCTCCTAGAGCTTGGGGTGGTCAGCAGCAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
/clone_lib="RAFL14"
/note="Site_1: BamHI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RAFL14-93-K05"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Urr
100.0%; Prr
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Pred. No. 1.8e-249;
0; Mismatches 0;
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AQ964580
AQ964580.1 GI:6792281
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
Tosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                           524;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Xiaoying Lin
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ964580 613 bp I
LERGX20TF LERG Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                Email: at@tigr.org
For addtional information,
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĊĠĠĠĠĊŔŦŦĊŔŔĠĊŦŔŔĊŔŦŔŦĊŦĠĠŦĊĠĠĠĠŔĊĠŔĠĊĠŦŦĠŔĠĊŔĠŔŔŔĠŦŔŦĠŔŦŔŔĊ
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                                                            ATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAAGAACGTTCAGGGTGGTTATAGGCCT
                GAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGACGAGACTGGCTTCTTCACAAGATGAT
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                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                    shotgun
                                                                                                                                                                                                       /clone lib="LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total
sheared to 0.4-0.7 Kbp before ligation."
                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                        clone="LERGX20"
                                                                                                                                          25.2%;
                                                                                                                           Score 474; DB 28;
Pred. No. 4.5e-230;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/at/at.html
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Best Local Similarity
Matches 379; Conserv
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

DNA Res. 7 (3), 175-180 (2000)

20363093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV525508 380 bp mRNA linear EST 01-SEP-2
AV525508 Arabidopsis thaliana aboveground organs two to six-week
old Arabidopsis thaliana cDNA clone APD25d02R 5', mRNA sequence.
AV525508
AV525508.1 GI:8685036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAAACACTTCTGGA 180
                                                                                                                                                                                                                                                                                                                     Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u> AAAACTTGGGGTTTCTCAGAATTCGAATCCTCCTAGAGCTTGGGGGTGGTCAGCAGCAAGGG</u>
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                                                                                                                                                                                                                                                                                        yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                        10907847
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                                                                                                             /tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana aboveground organs two to
six-week old"
                                                                                                                                                                                                          /mol_type="mRNA"
/strain="Columbia"
                                                                                                                                                                              /db_xref="taxon:3702"
/clone="APD25d02R"
                                                                                             note="Vector: pBluescriptII SK-;
                                                                                                                                                                                                                                           organism="Arabidopsis"
                                                                                                                                                                                                                                                                           ocation/Qualifiers
                    17.5%;
        <u>..</u>
      Score 329; DB 9;
Pred. No. 4e-156;
0; Mismatches 1
                                      Length
                                                                                                        Site_1:
             Indels
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EST 01-SEP-2000 o to six-week

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AUTHORS
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                                                                                                                                                                                                                                                                                         Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS00P9H 457 bp DNA linear GSS 28-JUN-199
Arabidopsis thaliana genome survey sequence T7 end of BAC F8G21 of
IGF library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                                                                                                                                                                                                                                                                                                                          Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P., Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
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AL084227
AL084227.1 GI:5
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                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                             Similarity
AGTGGCTCGGCATGGGCAACCAAGAGCTGCTGGAATACTTCGACAAGTATGAGGCTCTTA
                          AGTGGCTCGGCATGGGCAACCAAGAGCTGCTGGAATACTTCGACAAGTATGAGGCTCTTA
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                                                              15.7%; S
larity 100.0%;
Conservative 0;
                                                                                                                                             /clone_lib="IGF"
/note="end : T7"
                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="Columbia"
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                                                                                                                                                                             /clone="F8G21"
                                                                                                                                                                                            /db_xref="taxon:3702"
                                                                                                                                                                                                                                          organism="Arabidopsis thaliana"
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                                                              Score 295; DB; Pred. No. 9.8
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9.8e-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Unpublished (2000)
Contact: Xiaoying Lin
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
9712 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
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                                                                                                                                                                                             423;
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1 (bases 1 to 523)

1 (bases 1 to 523)

Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.

Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: TR
Class: shotgun.
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AQ959659.1 GI:6787360
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LEREM21TR LERE Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: at@tigr.org
For addtional information,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
                                                                                                                            GTCAGCAACAAGGGAGAGGTAGCAACGTATCTGGGAGAGGAAACAATGTATCCGGGAGAG
                                                                                      GTCAGCAGCAAGGGAGAGGTAGCAACGTATCTGGGAGAGGAAACAATGTATCCGGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGTGCCACTGGCTATTTGGAGGCCGAACGCCTCCACCGGGAGTTAGCTGAGATGGGGT 1141
 GTAACGGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCA
                  GTAACGGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCA 346
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                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                           /note=\overline{\mbox{"}}Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.6-0.8 Kbp before ligation."
                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="LANDSBERG ERECTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                               clone_lib="LERE"
                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
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                                                                                                                                                                                                             14.5%;
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                                                                                                                                                                                            Score 273; DB 28;
Pred. No. 1.8e-127;
0; Mismatches 3;
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    1635 TAATCCCTCTAGCAATGACGATTGCCGAAAGAGAGCTGAGGAAGTGTCAAGCTTCATCGA 1694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
Contact: Motoaki Seki
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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AU227277
                                                                                                                                                                                                                                                                                                                                                                                           Fax: 81-298-36-9060

Fax: 81-298-36-9060

Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially

An Arabidopsis full-length cDNA library was constructed essentially

An Arabidopsis full-length cDNA library was constructed with BamHI

as reported previously (Seki et al., 1998).cDNA cleaved with BamHI

and XhoI was ligated to modified the modified FLC-1 vector (Carninci et

al., submitted for publication) digested with BamHI and Sall. This

clone is in a modified pBluescript vector. Please visit our web

gite (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K., Doorth CDNA
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                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                           /clone_lib="RAFL14"
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                                                13.0%; Score 244; DB 9; 1
100.0%; Pred. No. 1e-112;
tive 0; Mismatches 0;
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Contact: Steve Rounsley
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
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Rounsley, S.D., Suh, E.J., Wible, C., Golden, K., Shatsman, S., Choi, P., Yu, K., Akinretoye, B., Shen, K., Goonasekaram, S., Militscher, J., Adams, M.D. and Venter, J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in A BAC End Sequence Database in Indate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                           /sex="hermaphrodite"
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Produced by Thomas Altmann"
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                                                                                                                                                                                                                                                                  Length 290;
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                                                                                                                                        Matches 169;
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1142 TAGATAGAATTGCCTGGGGTCAGAAGCGCAGTATGTTTTCTGGAGGTG 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,123
                                                                                      1710 GATGGAGGAGTTTGTGGAAGAGAGGGAGATGCTGATAAAAGATCAAGAGAAGAAGAAGATGGA 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouaroutoua, M., Myuyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Mobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A1999551
701556368 A. thaliana, Columbia Col-0, rosette-3 Arabidopsis thaliana cDNA clone 701556368, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: David Smoller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana Gene Expression MicroArray
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                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: service@genomesystems.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Systems, Inc., a wholly owned subsidiary of Incyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGTGCCACTGGCTATTTGGAGGCCGAACGCCTCCACCGGGAGTTAGCTGAGATGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314-427-3324
                                                                                                                                   Conservative
                                                                                                                                                                                                                                        /clone_lib="A. thaliana, Columbia Col-0, rosette-3"
/note="Vector: pSPORT; Site_1: NotI; Site_2: SalI; cDNA
library was derived from unitreated rosette tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1: peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was initiated
using a NotI-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to SalI adaptors, digested with NotI,
size-selected, and cloned into the NotI and SalI sites of
the pSPORT vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="rosette"
dev_stage="4 - 7 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Columbia Col-0"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="701556368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis thaliana"
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                                                                                                                                                           Score 169; DB 9;
; Pred. No. 2.2e-74;
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121
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                                                                                                                                110 CACAAGATGATGGAGGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAA 169
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                                                                                                                                                                                                                          50 GTTATAGGCCTGAGGTTGAACAGTTGGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
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A Sequence-Indexed Library of Insertion Mutations in the
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GSS.
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                            ACACTTCTGGAAAAACTTGGGTTTCTCAGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic D
/strain="Columbia 0"
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Pred. No. 2.3e-66;
153
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                     287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ecker@salk.edu
                                                                                                                       BH169448 482 bp DNA linear GSS 03-OCT-200 SALK 001377 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_001377, genomic survey sequence. BH169448
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryospermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                    BH169448.1
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/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines
/note="PCR was performed on Arabidopsis thaliana lines
/note="PCR was performed one or more TDNA insertion
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
the site of insertion.
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/strain="Columbia_0"
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pred. No. 1.1e-63;
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            Embryophyta; Tracheophyta;
edons; core eudicots;
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92
Tel: 858 453 4100 ×1752
Fax: 858 558 6379
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1 (bases 1 to 482)
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Unpublished (2001)
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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LERGX20TR LERG Arabidopsis thaliana
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                                                                                                                         Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
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                                                                                                                                                                                                                             Unpublished (2000)
                                                 Seq primer: TR
Class: shotgun
                                                                                                                                                                                                                                                     polymorphisms
                                                                                     Email: at@tigr.org
For addtional information,
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/clone=lib="Arabidopsis thaliana lines
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each of which contains one or more TDNA insertion
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
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Copyright (c) 1993 - 2004 Compus
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Sequence 27, Appl
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Sequence 130, Appl
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Sequence 7, Appli Sequence 1127, Ap	Sequence 2355, Ap	Sequence 4961, Ap	Sequence 1061, Ap	Sequence 594, App	Sequence 36, Appl	Sequence 940, App	Sequence 1728, Ap	Sequence 3, Appli	Sequence 16220, A	Sequence 10972, A	Sequence 1214, Ap	Sequence 1214, Ap	Seguence 1214, Ap	•	Sequence 767, App	Sequence 5, Appli

ALIGNMENTS

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; TYPE: DNA
; ORGANISM: Eucalyptus
US-09-615-192A-109
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Patent No. 6653528
GENERAL INFORMATION:
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Patent No., 6410718
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APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c2
CURRENT EPPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER APPLICATION NUMBER: US 08/7713,000
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
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NUMBER OF SEQ ID NOS:
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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tive (
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ORGANISM: Eucalyptus grandis
US-09-169-789-109
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NUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 109
LENGTH: 481
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                                                                            Query Match
Best Local (
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                                                              Matches
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
REPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
UMBER OF SEQUENCES: 88
ORDERSDANDENCT TOTALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                             TOPOLOGY:
                                                                                                                                                             LENGTH: 495 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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 484
                             74 TGGTTCAAGGTTTGGCAGG 92
                                                                 19;
                                                                                 Similarity
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   TGGTTCAAGGTTTGGCAGG 466
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                                                                 Conservative
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[00.0%; Pred. No.
                                                                 1.0%; Score 19; DB 2;
100.0%; Pred. No. 12;
tive 0; Mismatches
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                                                                                                                                                                                                                                  27:
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RESULT 4

US-09-041-075A-4

Sequence 4, Applicat Patent No. H002022 GENERAL INFORMATION:

Application US/09041075A

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APPLICANT:

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CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR PRILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 495
TYPE: DNA
GRGANISM: Eucalyptus grandis
US-09-615-192A-27
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                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-27
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RESULT 6
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bloksberg, Levier Applicant: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods
TITLE OF INVENTION; Modification of Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 27, Application US/09615192A
tent No. 6410718
                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: US 08/713,000
EARLIER FILING DATE: 1996-09-11
                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 11000.1003c2
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Materials and Methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%;
es 19; Conservative
                                                                                                                    Local Similarity
wes 19; Conserv
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                                                   484 TGGTTCAAGGTTTGGCAGG 466
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Havukkala, Ilkka
                                                                                     TGGTTCAAGGTTTGGCAGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09169789
                                                                                                                        Conservative
                                                                                                           100.0%; Pred. No.
100.0%; Mismatches
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00.0%; Pred. No.
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APPLICANT: Radding TITLE OF INVENTION: FILE REFERENCE: X-Patent No. H002022

Radding, Jeffrey A
VENTION: IPC SYNTHASE GENES FROM FUNGI
VCE: X-11242 Sequence Lst

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RESULT 8
US-09-595-684B-30
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SEQ ID NO 4
LENGTH: 2000
TYPE: DNA
ORGANISM: Candida kruisii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-041-075A-6
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                                                                                                                   Sequence 30, Application US/09595684B
Patent No. 6544766
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Ohashi, Cara
Applicant: Chashi, Cara
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6
LENGTH: 2000
TYPE: RNA
ORGANISM: Candida kruisii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. H002022
CURRENT APPLICATION NUMBER: US/09/041,075A
CURRENT FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/043,591
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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Best Local
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Heidler, Steven A
APPLICANT: Radding, Jeffrey A
TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/041,075A
CURRENT FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/043,591
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 24
                                                                                                        APPLICANT:
APPLICANT: Yu, Ming
TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: cytop036
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LOCATION: (300)..(1739)
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                                                                   Sakowicz, Roman
VAisberg, Eugeni
Wood, Kenneth
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Pred. No. 12;
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; LENGTH: 8257
; TYPE: DNA
; ORGANISM: Human
US-09-595-684B-30
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                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (91)..(8082)
US-09-620-312D-130
                                                                                                                                                                                                                                                                                                      APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 130, Application US/09620312D Patent No. 6569662
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Best Local
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CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
                                                                   Matches
                                                                                  Query Match
Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                  LENGTH: 8503
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                       FEATURE:
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les 19; Conserv
                                1802 TTGATCTGGAGAAAGAATT 1820
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2141 TTGATCTGGAGAAAGAATT 2159
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                                                                  19;
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Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Zhao, Qing A.
Wehrman, Tom
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Zhang, Jie
Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Jian-Rui
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                                                                   Conservative
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100.0%; Pred. No. 13
tive 0; Mismatches
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                                                                                     DB 4;
13;
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CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOPTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
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TITLE OF INVENTION:
FILE REFERENCE: PB275
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-916-421B-1
                                                  Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                            APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5315
LENGTH: 462
TYPE: DNA
                                                                                                                                                                                                                                                                                                                Sequence 5315, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t,
                                                                                                                                   ORGANISM: Klebsiella pneumoniae
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
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LOCATION: (1349491)..(1349491)
OTHER_INFORMATION: n equals a,
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LOCATION: (1603734)..(1603734)
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LOCATION: (1569020)..(1569020)
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OTHER INFORMATION: n equals a,
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RESULT 12 US-09-322-478-25/c ; Sequence 25, Application US/09322478

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HARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 25
LENGTH: 1254
TYPE: DNA
ORGANISM: Pisum sativum
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Best Local Similarity
Warches 18; Conserva
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                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 27805/3019
REFERENCE/DOCKET NUMBER: 27805/3019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Wigler, Mi
APPLICANT: Colicelli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -07-688-352C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURP Plant Retroelement
                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1829 base pair
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Street
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 199104 CLASSIFICATION: 435
STRANDEDNESS:
TOPOLOGY: lir
                                      TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                            TELEFAX:
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5527896
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                                                   1829 base pairs
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                                                                                                                               (312) 984-9740
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                                                                                           15:
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FEATURE:

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US-07-688-352C-15
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US-08-474
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                                                                                                        US-08-474-379C-15
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Best Local Similarity
                                                                                                                                                                                                                                                              PRIOR AFFICATION UNMBER: US 08/206,188
APPLICATION UNMBER: US 07/688,352
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
PILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 3127
TELECOMMUNICATION INFORMATION:
TELEPHANE: (312) 474-6300
TELEPHAN: (312) 474-6300
TELEPHAN: (312) 474-0448
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                               Best Local Similarity Matches 18; Conserv
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                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                               FEATURE:
                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/474,379C FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Illinois
COUNTRY: United States of America
                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
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                                                                                                                                                                                                  TOPOLOGY:
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   139 ATTTCCAAGAAGAACAAG 156
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                                                                                                                                                                                                                                  nucleic acid
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233 South Wacker Drive/6300 Sears Tower
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                             1.0%; inilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                       1829 base pairs
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100.0%; Pred. No.
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0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511
PILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107

US 07/511,715

SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/146,249

US/09/146,249A

Version #1.25

FILING DATE: CLASSIFICATION:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

TELEX: 25-3856
INFORMATION FOR SEQ ID NO:

15:

SEQUENCE CHARACTERISTICS: LENGTH: 1829 base pair

LENGTH: 1829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE:

TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300

312-474-0448

TELEPHONE: TELEFAX:

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                                                                                                                                                                                                                                                    RESULT 15
US-09-146-249A-15
                                                                                                                                                                                                           Patent No. 6069240
GENERAL INFORMATION:
                                                                                                                                                                                                                                        Sequence 15,
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                  APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by
TITLE OF INVENTION: Processes
                                                                                                                       NUMBER OF SEQUENCES: 8:
                                                                STREET: Chicago
                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                              286
                                                                                                                                                                                                                                                                                                              Illinois
                                                                                                                                                                                                                                        Application US/09146249A
                                                                                           6300 Sears Tower,
                                                                                           Marshall, O'Toole,
                                                                                                                                                                  Michael H.

li, John J.

Cloning by Complementation and Related
                                                                                             Gerstein, Murray & South Wacker Drive
                                                                                                                 Borun
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NAME/KEY: ; LOCATION: US-09-146-249A-15 밁 S Matches Query Match Local Similarity 139 ATTTCCAAGAAGAACAAG 156 985 ATTTCCAAGAAGAACAAG 1002 18; CDS 30..1421 Conservative 100.0%; 1.0%; 0; Score 18; ; Pred. No. Mismatches DB 3; 0; Length 1829; 0 Gaps 0

Search completed: April 9, 2004, 08:20:46 Job time : 96.5698 secs

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Minimum
Maximum
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/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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US-10-424-599-91176
US-10-085-783A-19246
US-10-242-535A-19246
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US-10-27-633-293476
US-10-174-693-27
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Sequence 91177, A
Sequence 19176, A
Sequence 19246, A
Sequence 19246, A
Sequence 27937, A
Sequence 293476,
Sequence 203, App
Sequence 27, Appl
Sequence 167, App
Sequence 1849, A
Sequence 23556, A
Sequence 23556, A
Sequence 11811, A
Sequence 11812, A
Sequence 24736, A
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US-09-960-352-3954	US-09-960-352-12961	US-09-728-445-290	US-10-424-599-112786	US-09-960-352-14374	US-10-424-599-116017	US-09-960-352-12756	US-09-864-761-32008	US-10-029-386-26108	5 US-10-027-632-174763			US-10-085-117-145	US-10-117-722-130	US-10-037-270-130	US-10-071-766-51	US-10-133-013-260	US-09-893-519A-140	US-09-770-107-1	US-10-176-847-9	US-10-108-260A-1451	US-09-742-581-6	US-09-742-581-4	US-09-742-580-6	US-09-742-580-4	US-09-742-582-6	US-09-742-582-4	US-10-424-599-4367	US-09-938-842A-2465	US-09-938-842A-2465
Sequence 3954, Ap		Sequence 290, App	Sequence 112786,	Sequence 14374, A	Sequence 116017,	Sequence 12756, A	Sequence 32008, A	Sequence 26108, A	Sequence 174763,	Sequence 1, Appli		145,	Sequence 130, App	130,	51, /	Sequence 260, App		Sequence 1, Appli	Sequence 9, Appli		ο,	4	φ,	e 4,	Seguence 6, Appli	Sequence 4, Appli	Sequence 4367, Ap	e 2465,	Sequence 2465, Ap

ALIGNMENTS

US-10-424-599-91177

Sequence 91177, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J APPLICANT: Kovalic David K

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US-10-424-599-91176, Application US/10424599; Sequence 91176, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 91177
LENGTH: 1377
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                    Query Match
APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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SEQ ID NO 91176
                                                                                                                                                                                                                                   US-10-242-535A-19246
                                                                                                                                                                                                                                                       RESULT 4
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Best Local Similarity 100.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT3847_53342C.1
-10-424-599-91176
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                       Sequence 19246, Application US/10242535A Publication No. US20040013663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ChondroGene Inc. APPLICANT: Liew, C.C.
                                     APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
CURRENT FILING DATE: 2002-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
                                                                                                                           APPLICANT: ChondroGene Inc. APPLICANT: Liew, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 58994
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PRIOR APPLICATION NUMBER: US 10/085,783 PRIOR FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
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Zhou Yihua
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GENERAL INFORMATION:

GENERAL INFORMATION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FAILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483
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                                                                                                                                                                                                                                                                                                                                                                     US-10-027-632-293476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.2 SEQ ID NO 19246
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Best Local :
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 57837, Application US/10424599 Publication No. US20040031072A1
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                    Sequence 293476, Application US/10027632 Publication No. US20030204075A9
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APPLICANT: Kovalic David K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/271,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1700 AAGAGAAAGAGATGGAGGA 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 AAGAGAAAGAGATGGAGGA 280
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; Pred. No.
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RESULT 8
US-10-174-693-27/c
; Sequence 27, Application US/10174693
; Publication No. US20030131373A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Eucalyptus grandis US-10-174-693-109
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CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR FILING DATE: 2000-07-12
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SEQ ID NO 109
LENGTH: 481
                                                                                                                                                                                                                                                                                                                                                                                    Matches
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 293476
LENGTH: 429
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Best Local Similarity
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APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003C5
CURRENT APPLICATION UNDERS: US/10/174,693
CURRENT FILING DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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les 19; Conser
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100.0%; Pr
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100.0%; Pred. No.
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Pred. No.
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47;
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US-10-424-599-18549/c
; Sequence 18549, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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; ORGANISM: Eucalyptus grandis
US-10-174-693-27
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PRIOR FILING DATE: 1997-11-21
PRIOR PELICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 407
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 167
LENGTH: 501
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Best Local Similarity
Matches 19; Conserv
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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Best Local Similarity
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
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; Pred. No.
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47;
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47;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_116754C.1
US-10-424-599-18549
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PRICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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; ORGANISM: Human
US-10-027-632-23555
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                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-027-632-23556/c
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Best Local Similarity
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SEQ ID NO 23555
LENGTH: 696
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Sequence 23556, Application US/10027632
Sequence 23556, Application US/0027632
Publication No. US20030204075A9

GENERAL INFORMATION:
GENERAL INFORMATION: David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTICUS: Polymorphisms in the Human Genome
PILE REFERENCE: 108827.129
PILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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SOFTWARE: FastSEQ for Windows Version 4.0
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nes 19; Conservative
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US-10-027-632-11811
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PRIOR PELLING DATE: 2000-07-12

PRIOR PELLING DATE: 2000-07-12

PRIOR PELLING DATE: 2000-04-20

PRIOR PELLING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PELLING DATE: 2000-03-29

PRIOR PELLING DATE: 2000-03-29

PRIOR PELLING DATE: 2000-02-24

PRIOR PELLING DATE: 2000-02-24

PRIOR PELLING DATE: 1999-11-23

PRIOR PELLING DATE: 1999-11-23

PRIOR PELLING DATE: 1999-11-23

PRIOR PELLING DATE: 1999-01-28

PRIOR PELLING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PELLING DATE: 1999-08-09

PRIOR PELLING DATE: 1999-08-09

PRIOR PELLING DATE: 1999-08-09

PRIOR PELLING DATE: 1999-08-09
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US-10-027-632-11811
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LENGTH: 696
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR PRIOR PRICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                 SEQ ID NO 11811
LENGTH: 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
                                                                                                                               Query Match
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FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/185,218
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100.0%; Pred. No.
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RESULT 14 US-10-027-632-11812 . sequence 11812, Application US/10027632

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US-10-369-493-24736

Sequence 24736, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2008-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1909-11-23
PRIOR PRILOR DATE: 1909-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-28
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF ESO ID NOS: 47374
SEQ ID NO 24736
LENGTH: 1137
TYPE: DNA
ORGANISM: Methanococcus jannaschii
US-10-369-493-24736
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SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 11812
LENGTH: 824
TYPE: DNA
GRGANISM: Human
US-10-027-632-11812
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607 GAGAAAGAGATGGAGGAGT 625
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	σ	4.	w	2	1	No.	Result
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Abm64162 Propionib	Aau67643 Propionib		Abm38151 Propionib	Aau41632 Propionib	Aam89334 Human imm	Abp08249 Human ORF			Abm40365 Propionib	Aau43846 Propionib	Aao18207 Murine ro	_	Aab13241 Caenorhab	Aao04467 Human pol	<u>'</u>	Abp82841 G protein	Abg71491 Prostatic	Aae19162 Human kin	Adc99064 Human KPP	Abu23489 Protein e	Aab18189 Plasmodiu	ဂ္ဂ	Aag91534 C glutami	Aab31798 Amino aci	Description	

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Abp56866	Aab76573	Abm52952	Aau56433	Aau99286	Abg29097	Ade52649	Abg19350	Abu23918	Abp71173	Abp71172	Abp71174	Abp71171	Abg16117	Abm62707	Aau66188	. Abg71490	Ade45844	Aau21876	06 / Folligh
Mouse CIT	Corynebac	Propionib	Propionib	Rotavirus	Novel hum	Murine dn	Novel hum	Protein e	Mouse pro	Rat pro-N	Chicken p	Human pro	Novel hum	Propionib	Propionib	Human pro	Human car	Human car	הדיות ביות

ALIGNMENTS

RESULT 1 AAB31798 ID AAB3 XX AAB3 XX AAB3 XX AAB3 XX AAB3 XX AAB3 XX YOU DE Amin XX SGS3 XW Vira XX WO20 XX Arak XX Arak XX Hole PN WO20 XX 16-1 PF 13-1 XX INI XX 16-JUL-1999; 99FR-00009417. 26-JAN-2000; 2000FR-00001006. 13-JUL-2000; 2000WO-FR002052. 25-JAN-2001. WO200105951-A2. Arabidopsis thaliana. SGS3 gene; post-transcriptional inactivation; RNA degradation; viral resistance; resistance; fatty acid content; protein content. Amino acid sequence of the Arabidopsis SGS3 polypeptide 15-MAY-2001 AAB31798; AAB31798 standard; protein; 625 (first entry) Ą

New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene expression.

(AVET)

AVENTIS CROPSCIENCE SA.
INST NAT RECH AGRONOMIC

AGRONOMIQUE. Vaucheret H;

Beclin C,

Elmayan T,

WPI; 2001-159529/16. N-PSDB; AAF25374.

Claim 8; Fig 1; 36pp; French.

The gresent sequence represents an Arabidopsis thaliana SGS3 polypeptide. The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased resistance to viruses, while inactivation of SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous recombination) increases the level of the transgene product. This product may e.g. impart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active, e.g. an immunoglobulin or interferon

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                                                                                                                                         Corynebacterium
                         18-DEC-2000; 2000EP-00127688
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03-AUG-2000;
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25-JUN-199;
08-JUL-1999;
09-JUL-1999;
09-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum, homeostasis; adaptation; HA protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering; Brevibacterium; environmental condition.
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DB; AAH66753.
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; 2000JP-00280988.
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99DE-01031636.
99DE-01032125.
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Ikeda M, Ozaki A;
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(I) can be used to map the C. glutamicum genome or can be used as markers for genetically engineered Corynebacterium or Brevibacterium. The HA proteins encoded by the (I) are used to maintain homeostasis in C. conditions or help the microorganism to adapt to different environmental
                                                                                                                                                                                        Matches
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N-PSDB; AAF71292.
                                        AAB18189;
                                                                  AAB18189 standard;
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                   19-JUN-2003
                                                                                   ABU23489
                                                                                                                    ABU23489 standard; protein; 916
                                                                                                                                                                                                                                                                                                                                          Sequence 483 AA;
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33 ISKKNKNK 40
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rative 0; Mismatc
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protozoacide;
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Protein encoded by Prokaryotic essential gene #9016.

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the invention relates to an isolated multiplication where expression of the mucleic acid inhibits proliferation of a cell. Also included are: confirmed the nucleic acid inhibits proliferation of a cell. Also included are: confirmed to expression is inhibited by the antisense concluded; (2) a host cell containing the vector; (3) an isolated content comprising a promoter operably linked to the nucleic acid content whose expression is inhibited by the antisense content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content content
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                            Sequence
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DB; ACA27359.
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02-NOV-2001; 2001US-0343910P.
13-NOV-2001; 2001US-033908P.
16-NOV-2001; 2001US-0332424P.
30-NOV-2001; 2001US-0334288P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2002; 2002WO-US033723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                  The invention relates to a novel isolated polypeptide which is a huma kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or agonists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, preventing cell proliferative disorders such as therosclerosis, and cancer, developmental disorders e.g. mental cirrhosis, hepatitis and cisorders including Alzheimer's disease and retardation, neurological disorders including Alzheimer's disease and Parkinson's disease, autoimmune and inflammatory disorders such as Parkinson's disease and diabetes mellitus and finally, viral, bacterial, frungal, parasitic, protozon or helminthic infections. Furthermore, to polynucleotides encoding KPP may be useful for creating transgenic procedures. The current sequence is that of the human KPP protein of incortions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gururajān R, Hafalia AJA, Khan FA Lindquist EA, Lu DAM, Lu Y, Marz Ramkumar J, Recipon SA, Richardso Thornton MB, Tran UK, Chawla NK, Zebarjadian Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADC99116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
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Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 17; 424pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Becha SD, Borowsky ML, Duggar
IJ, Gandhi AR, Gorvad AE, Gri
AJA, Khan FA, Lal PG, Lee EA,
Lu Y, Marquis JP, Nguyen DB,
Lu Kichardson TW, Swarnakar A,
Chawla NK, Warren BA, Yang J
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g, Griffin
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Tang YT;
Yao MG, Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JA;
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Sequence 1553 AA;

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AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1917 AAE1
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Best Local Similarity
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New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2000; 2000US-0220038P.
28-JUL-2000; 2000US-0222112P.
04-AUG-2000; 2000US-0222831P.
11-AUG-2000; 2000US-0224729P.
                                                                                                                                                                                    Tribouley CM, Ba
Yao MG, Elliott
Tang YT, Xu Y,
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                                                                                                         WPI; 2002-206083/26.
N-PSDB; AAD30567.
                                                                                                                                                                                                                                                                                          Thornton M,
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                                                                                                                                                                                                                                                                                          Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide (PKIN-20).
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                                                                                                                                                                         Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK;
Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding
Ott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "CNH domain"
1100. .1380
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o. 1.5e+02;
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2000; 2000CN-00127237.
                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2000; 2000CN-00127237.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haemopathy; human immunodeficiency virus; HIV; immunological disease; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostatic specific membrane antibody protein 11.88; antibody; prostatic cancer; prostatic benign tumour; folic acid; metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostatic specific membrane antibody protein 11.88 N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1572 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to an isolated human kinase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 170-174; 196pp; English
                                                                                                                                                                                                                                                                                                                       (BODE-)
                                                                                                                                                                                         2002-692403/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 RLHRELAE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493 RLHRELAE 500
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                                                                                                                                                                                                                                                     Xie
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8; Conserv
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b. 1.5e+02;
ches 0; Indels
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New human prostatic specific membrane antibody protein 11.88 polypeptide for treating e.g. prostatic cancer, folic acid metabolic fault, human

immunological diseases,

immunodeficiency virus infection,

Chinese.

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the human prostatic specific membrane antibody protein 11.88, a polynucleotide encoding the polypeptide and a DNA recombination process used to produce the polypeptide. The polypeptide and the polynucleotide are used for treating various diseases, such as prostatic cancer, prostatic benign tumour, other tumours, folic acid metabolism fault, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and inflammations. This sequence represents a human prostatic specific membrane antibody protein 11.88 Netreminal peptide, used in EDISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; g protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporrosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 AA;
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-2003
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                                                                                                              Claim 1; Fig
                                                                                                                                                                                                                                                                             Burmer GC,
                                                                                                                                                                                                                                                                                                                                                  19-DEC-2000; 2000US-0257144P
                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-coupled receptor
                                                                                                                                                              w isolated antigenic peptides e.g., for G protein-coupled receptors PCR), useful for diagnosing and designing drugs for treating conditions which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                           2003-046718/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 SKKNKNK 54
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                                                                                                                                                                                                                                                                             Roush
                                                                                                                                                     diseases.
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                                                                                                              2; 523pp;
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                                                                                                                                                                                                                                                                                                                  BIOSCIENCES INC
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                                                                                                                English.
                                                                                                                                                                                                                                                                               Brown JP
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Pred. No.
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Example 1;

50;

95pp; English. transcription

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discloses Page

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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE12564 standard; peptide;
                                                                                                                                                       New transcription transactivator protein of CITED family, termed HCITEDX, useful for controlling hypoxia signaling, inflammation, activating cholesterol uptake genes and identifying compounds interfering with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-2000; 2000GB-00006572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis; atopic disease; cytostatic;
p35srj/CITED2 p300-CH1 interacting domain.
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                                                                                                                                                                                                                                                                                                                                                           Bhattacharya S,
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CC and its corresponding polymucleotides. HCITEDX proteins are useful for
CC identifying compounds which modulate the cytroplasmic sequestration of the
CC identifying compounds which modulate the cytroplasmic sequestration of the
CC in the activation of genes involved in cholesterol uptake, cholesterol
CC biosynthesis and in the control of inflammation. They are therapeutically
CC useful in number of different indications, particularly reduction of
CC cholesterol biosynthesis and inflammation, prevention of tumour
CC angiogenesis and treatment of any other condition. HCITEDX proteins are
CC useful in screening methods for identification of compounds which
CC interfere with the function of HCITEDX and useful for modulating hypoxia
CC signalling, tumour angiogenesis or cholesterol synthesis. HCITEDX
CC modulators are useful for preventing tumour angiogenesis and treating
CC ischaemic heart disease. Compounds which promote the translocation of
CC cytoplasmic HCITEDX in breast cancer cells are useful as leads in the
CC development of anti-breast cancer rells are useful as leads in the
CC development of anti-breast cancer rells are useful as leads in the
CC modulators are useful for treating Netherton's disease or atopic disease.
CC modulators are useful for treating Netherton's disease or atopic disease.
CC modulators are useful for used in gene therapy. The present peptide
CC sequence is the p300-CH1 interacting domain of p35srj/CITED2. This
CC sequence is used to clone full length HCITEDX
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Best Local
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                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                    N-PSDB; AAI84398
                                                                                                                                                                                                                                                                Tang YT,
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18-MAY-2000; 2000US-00577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US004927.
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Similarity 100.0%; P:
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Pred. No.
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The invention relates to human polynucleotides (AAI79941-AAI93841) and

Claim 20; SEQ ID NO 18359; 1399pp + Sequence Listing; English

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Best Local Similarity
Matches 7; Conser
The present sequence is conserved protein region of a Caenorhabditis elegans homologue of a key metabolic enzyme. A number of C. elegans genes have been identified as homologues of genes in the mammalian insulin signalling pathway. The C. elegans age-1 gene encodes a homologue of the mammalian PI 3-kinase whilst daf-2 encodes a homologue of the mammalian insulin receptor. The C. elegans AKT kinase and PKB kinase act downstream of daf-2 and age-1, just as their mammalian homologues act downstream of insulin signalling. The C. elegans PTEN lipid phosphatase homologue, DAF-18, has been found to act upstream of AKT in the pathway. This discovery has enabled mammalian PTEN action to be mapped to the insulin signalling pathway. Conserved DAF motifs can be used to design probes to identify mammalian DAF homologues and thus to identify individuals with a predisposition toward the development of glucose intolerance conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the encoded proteins (AAOO0010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans; metabolic enzyme; AKT kinase; daf-18; insulin signalling pathway; daf-2; age-1; insulin receptor; PI 3-kinase; PKB kinase; PTEN lipid phosphatase; antidiabetic; anorectic; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 167; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity.
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine rotavirus non-structural protein 4 NSP4 fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel crystal of oligomerization domain of rotavirus nonstructural protein 4, useful for determining 3 dimensional crystal structure of the domain that is used for identifying agents which interact with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel crystal of oligomerization domain of rotavirus nonstructural protein 4, useful for determining 3 dimensional crystal structure of domain that is used for identifying agents which interact with the
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                               21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                 SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes immunogenic protein #4742
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                               ; 2000US-0199047P.
; 2000US-0208841P.
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                                                                                                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies pecific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and CC diagnostic agents for determining P. acnes proteins. The antibodies may also be used as CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was contacton electronic format directly from WIPO at
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                Sequence 51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
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N-PSDB; AAS59521.
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L'maisonneuve J, Zhang Y,
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                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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Compugen Ltd

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Result
No.
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Maximum DB
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
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625
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Match
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probable uroporphy
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A;Residues: 1-353 <MAG>
A;Cross-references: EMBL:AF101310; PIDN:AAC69214.1; GSPDB:GN00023; CESP:C39F7.5
A;Experimental source: strain Bristol N2; clone C39F7
C;Genetics:
A;Gene: CESP:C39F7.5
A;Gene: CESP:C39F7.5
A;Map position: 5
A;Introns: 14/2; 45/3; 224/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C39F7.5 R;Maggi, L.; Scheet, P.; Dubbelde, C. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid C39F7. A;Reference number: Z21407 A;Accession: T33782 A; Molecule type: DNA
A; Residues: 1-603 <HAL>
A; Residues: 1-603 <HAL>
A; Cross-references: EMBL: UZ9380; PIDN: AAA68747.1; CESP: ZK546.13
A; Experimental source: strain Bristol N2
C; Genetics: hypothetical protein ZK546.13 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27901 RESULT 1 T27901 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA hypothetical protein C39F7.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T33782 밁 S A;Accession: T27901 A;Status: preliminary; translated from GB/EMBL/DDBJ R;Hallsworth, K.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid ZK546.
A;Reference number: Z20437 A; Gene: CESP: ZK546.13 A; Introns: 26/3; 111/ Query Match
Best Local Similarity
Matches 9; Conserv Query Match 469 LEIMSEKLR 477 433 LEIMSEKLR 441 26/3; 111/3; 196/3; 275/3; 331/1; 362/3; 438/3; 500/3 Conservative 100.0%; F rative 0; 1.4%; Score 9; DB 2 100.0%; Pred. No. 1.5 ive 0; Mismatches 1.3%; Score 8; DB 2; DB 2; Length 353; Length 603; <u>,</u> Indels 0 Gaps 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PFB0235w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001382;
A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C18E9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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snRNP homolog [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001
C;Accession: G84303
                                                                                                                                                                                                                                                                                          A;Map position: 2
A;Introns: 158/3; 269/3; 354/3; 493/2; 538/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C18E9
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Matches
                                                                        G84303
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Matches 8
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8; Conservative (
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; St
llarity 100.0%; I
Conservative 0;
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Conservative
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[00.0%; Pred. No. 16;
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                        02-Feb-2001 #text_change 02-Feb-2001
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A;Gene:
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                                                                                                                    A,Title: The complete genome of the hyperthermophilic bacterium A,Reference number: A70300; MUID:98196666; PMID:9537320 A,RACCession: B70456
                                                                                                                                                                                                                                 thioredoxin - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Accession: B70456
C;Accession: B70456
C;Accession: B70456
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                 A, Experimental source: strain VF5 C; Genetics:
                                                   A;Molecule type: DNA
A;Residues: 1-135 <AQF>
A;Residues: 1-135 <AQF>
A;Cross-references: GB:AE000757; NID:g2984092; PIDN:AAC07635.1;
                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not
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G.; Warren, P.V.; Gaasterland,

T.; Young,

W.G.; Lenox,

A.L.; Graham,

D.E., ş

Aquifex aeolicus

PID:g2984097; GB:AE00065

Aquifex aeolicus

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Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A, Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, A; Reference number: A84160; MUID:20504483; PMID:11016950

A, Accession: G84303

A. Accession: G84303
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                                                                                                                                                                                                                                                                                              Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omex, A.D.; A; Title: Genome sequence of Halobacterium species NRC-1. A; Reference number: A84160; MUID:20504483; PMID:11016950 A; Accession: D84164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng0041c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE004437; NID:g10580991; PIDN:AAG19795.1; GSPDB:GN00138
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A; Residues: 1-69 <STO>
                                                                                                                                                        A; Gene: VNG0041C
C; Superfamily: Ha
                                                                                                                                                                                                 A;Cross-references: GB:AE004437; NID:g10579692; PIDN:AAG18680.1; C;Genetics:
                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-101 <STO>
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55 AHARTKG
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25;
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o. 36;
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; Maddocks, D.
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ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI2669
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J. Bacteriol. 183, 4823-4838, 2007.
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97338
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A;Residues: 1-145 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43375.1; PID:g17740871; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
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A; Residues: 1-141 < KUR>
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A;Cross-references: EMBL:M10138; NID:g171294; PIDN:AAA66900.1; PID:g171295
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cytochrome-c oxidase (EC 1.9.3.1) chain VI precursor - yeast (Sa N;Alternate names: protein H8179.2; protein YHR051w C;Species: Saccharomyces cerevisiae c;Pate: 13-Jun-1983 #sequence_revision 31-Dec-1992 #text_change C;Accession: A22853; S46730; A00494; S48874 R;Wright, R.M.; Ko, C.; Cumsky, M0494; Poyton, R.O. J. Biol. Chem. 259, 15401-15407, 1984 A;Title: Isolation and sequence of the structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal structural gene for cytocal stru
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A;Residues: 1-147 <HEL>
A;Residues: 1-147 <HEL>
A;Residues: 1-157 <MID:940798; PIDN:CAA46012.1;
A;Experimental source: strain ATCC 29494
G;Superfamily: flavodoxin; flavodoxin homology
C;Superfamily: flavodoxin; flavoptorein; FMN
E;6-143/Domain: flavodoxin homology <FLX>
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A; Residues: 1-148 < WRI>
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A; Residues: 1-147 < KUR>
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Biochim. Biophys. Acta 1131, 325-328, 1992
A;Title: The primary structures of the flavodoxins from
                                                                     A; Accession: A22853
                                                                                                       A; Reference number: A92466; MUID: 85080033;
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C;Date: D=Dec-1997 #sequence_revision O5-Dec-1997 #text_change 20-Jun-2000
C;Date: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 20-Jun-2000
C;Accession: D69831
C;Accession: D69831
R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertel
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
C; Bron, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Entian, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Entian, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Aluthors: Fouliger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A.; Aluthors: Lauber, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A.; Mathors: Lauber, J.; Lazarevic, V.; Lee, S.; M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
A.; Mathors: Schleich, S.; Schroeter, R.; Scuffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
A.; Britle: The complete, A.; Tanaka, T.; Terpstra, P.; Sekiguchi, J.; Sekowska, A.; Serot
A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Togato, V.; Uchiyama, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A.; Alceusion: D69831
A.; Accession: D69831
A.; Accession: D69831
A.; Cross-references: GB:Z99109; GB:AL009126; NID:92633260; PIDN:CAB12871.1; PID:92633367
A.; Cross-references: GB:Z99109; GB:AL009126; NID:92633260; PIDN:CAB12871.1; PID:92633367
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A; Residues: 1-148 <DUZ>
A; Residues: 1-148 <DUZ>
A; Residues: 1-148 <DUZ>
A; Cross-references: EMBL: U00062; NID: 9488162; PIDN: AAB688
A; Cross-references: EMBL: 13087, 1982
J. Biol. Chem. 257, 13081-13087, 1982
J. Biol. Chem. 257, 13081-13087, 1982
A; Title: The amino acid sequence of cytochrome c oxidase A; Reference number: A00494; MUID: 83030850; PMID: 6290493
A; Accession: A00494
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A; Reference number: S46732
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Nucleic Notation and expression of the COX6 genetic locus A;Title: Organization and expression of the COX6 genetic locus A;Teference number: S48872; MUID:89160242; PMID:2537949
A;Accession: S48874
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A; Residues: 41-148 < GRE>
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A;Map position: 8R
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A;Residues: 1-23 <WRW>
A;Cross-references: EMSL:X14452; NID:g3573; PIDN:CAA32622.1;
C;Comment: Cytochrome-c oxidase is the terminal component of
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
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7; Conservat
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he sequence of S. cerevisiae
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nilarity 100.0%;
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%; Pred. No. 51;
0; Mismatches
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the respiratory chain;
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A;Gene: yhfO
C;Superfamily: Methanococcus
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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C. A;Authors: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, C. A;Buthors: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Fitle: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A98039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical exported protein, glycine-rich [imported] - Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Datc: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endot A;Reference number: A95842; MUID:21396508; PMID:11481431
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                                                                                                                                                                                                                                                                                            hypothetical protein T23C6.4 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te C.Accession: T15118
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A;Molecule type: DNA
A;Residues: 1-152 <KUR>
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A;Accession: T1511P
A;Srah...
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There 7; Conserve
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A;Genome: plasmi
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A;Gene: CESP:T23C6.4
A;Map position: X
A;Introns: 37/1; 90/1; 142/2
C;Superfamily: Caenorhabditis
                                                                                                       A;Cross-references: EMBL;AF000191; NID:g1946976; PID:g1946981; A;Experimental source: strain Bristol N2; clone T23C6
                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-182 < DUZ>
                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid T23C6
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7; Conserv
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         elegans hypothetical protein T23C6.4
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; Pred. No. 52;
0; Mismatches
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; Fisher, R.F.,
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O9zjj7 helicobacte
O9ukp3 homo sapien
O8uin5 agrobacteri
O92st0 rhizobium m
P54918 synechocyst
O87816 vibrio para
O8dez8 vibrio vuln
O7v6b8 prochloroco
O60478 homo sapien
Q7vga7 helicobacte
                                                                                                                                                                                                                                                       Q8ng33 corynebacte
Q8eqt oceanobacil
Q9rda9 clostridium
Q01096 desulfovibr
P00427 saccharomyc
Q25537 sarcophaga
Q95150 cervus elap
Q9wyk4 thermotoga
P25433 gallus gall
Q9tst2 felis silve
P20783 homo sapien
P20181 mus musculu
P18280 rattus norv
Q35740 mus musculu
P18280 rattus norv
Q35740 mus musculu
Q8fi04 escherichia
P24209 escherichia
P25633 saccharomyc
P32773 saccharomyc
P32814 bacillus st
P25693 saccharomyc
P35614 helicobacte
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RESULT 2
RBFA_OCEIH

ID RBFA_OCEIH

STANDARD; PRT; 113 AA.

AC OBEOT9;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ribosome-binding factor A.

GN RBFA OR OB1600.

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179 DSDALDDSD 187

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170	Query Match Best Local Matches	EMBL; AP005279 HAMAP; MF 0007: InterPro; IPR0(Pfam; PF01029; Transcription (SEQUENCE 227	he he he he he he he he he he	Nakagawa S. "Complete g: Submitted () -i- FUNCTIO: -i- SIMILAR	Corynebacterium gl. Bacteria; Actinoba Corynebacterineae; NCBI_TaxID=1718; [1] [1] SEQUENCE FROM N.A.	Qen(33; 28-FEB-2003 (Rel 28-FEB-2003 (Rel 28-FEB-2003 (Rel N utilization su	LT 1 CORGL NUSB CO		44440 543210	2 2 3 3 4 4 4 5 6 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6
	h Sim 9;	AP005279; MF_00073 PF01029; PF01029; Pription to the control of the control o	is SWISS-PROT ween the Swi European Bio by non-pro diffed and thi ities require send an email	gawa S.; glawa S.; plete genomi itted (MAY-2 FUNCTION: In similarity). SIMILARITY:		2003 2003 2003 2003 zatio	CORGL		111111	11111
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178	1. 100 :ive	9011. 1. NusB 1. ation 25010	itry is copyrig Institute of Institute of Informatics Institution it institution statement is nealicense agree a license@isb-	ic sequence of 2002) to the El nvolved in the Belongs to the	tamicum (Brevibacter teria; Actinobacter Corynebacteriaceae;	41, Creat 41, Last 41, Last stance pro	STANDARD;		528 528 528 529	453 461 476 483 510
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	9; DB 1; No. 0.26; matches	te proteome. 5A070B52342A5	ormatic There ong as oved. (See ht	bacterium Bank/DDBC ription t	rium idae Cor	NNV3.3; 8-PEB-2003 (Rel. 41, Created) 8-PEB-2003 (Rel. 41, Last sequence update) 8-PEB-2003 (Rel. 41, Last annotation update) utilization substance protein B homolog (Nusbush or CGI-618	227 AA.	ALI GNMENTS	RAT HUMAN HUMAN MACFA MACFA MACFA MACFA	ECOLI SYNY3 YEAST YEAST HABIN
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RESULT 3
FABZ_CLOAB
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Matches 8; Conserv
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STRAIN-HTE831 / DSM 14371 / JCM 11309;

MEDIJINE-22220767; PubMed-12235376;

Takami H., Takaki Y., Uchiyama I.;

"Genome sequence of Oceanobacillus ineyensis isolated from the Ridge and its unexpected adaptive capabilities to extreme Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oceanobacillus iheyensis.
Bacteria, Firmicutes; Bacillales;
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 30:3927-3935 (2002).

Nucleic Acids Res. 30:3927-3935 (2002).

PUNCTION: Associates with free 30S ribosomal subunits (but not refunction).

With 30S subunits that are part of 70S ribosomes or polysomes).

Essential for efficient processing of 16S rRNA, May interact with Essential helix region of 16S rRNA (By similarity).

The 5'terminal helix region of 16S rRNA (By similarity).

-1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP004598; BAC13556.1; -.

HAMAP; MF 00003; -; 1.

InterPro; IPR000238; Rib_bind_factA.

Pfam; PP02033; RBFA; 1.

ProDom; PD007327; Rib_bind_factA; 1.

TIGRPAMS; TIGR00082; TbfA; 1.

PROSITE; PS01319; RBFA; 1.

TRUA processing; Complete proteome.

TRUA processing; Complete proteome.

TRUA DECCESSING; Complete PROSITE; COMPLETE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
(3R)-hydroxymyristoyl-facyl carrier protein)
((3R)-hydroxymyristoyl ACP dehydrase).
FABZ OR CAC3571.
                                                                                   SEQUENCE FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325 / DubMed=11466286;

MODELINE-21359325 / DubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zen, Moling J., Dubois J., Qiu D., Hitti J., Wolf Y.I.

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., I.

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-pr
bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium
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                                J. Bacteriol. 183:4823-4838(2001)
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1488;
           SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLOAB
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           saturated fatty
Cytoplasmic (By
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01-APR-1993 (Rel. 2
01-APR-1993 (Rel. 2
10-OCT-2003 (Rel. 4
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HAMAP; MF 00406; -; 1.
InterPro; IPR006683; Thioestr_supf.
Pfam; PF03061; 4HBT; 1.
Lyase; Lipid synthesis; Lipid A biosynthesis; Complete proteome.
Lyase; Lipid synthesis; Lipid A biosynthesis; Complete proteome.
ACT_SITE 49 49 BY SIMILARITY.
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desulfovibrio gigas.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The primary structures of the flavodoxins from two strains besulfovibrio gigas. Cloning and nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come and the statement is greenent (See http://www.isb-sib.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.ch/and.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 29494 / DSM 496;
MEDLINE=92329549; PubMed=1627649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flavodoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a . between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: FMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helms L.R., Swenson R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=879;
                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - |- FUNCTION: Low-potential
                                                                                                                                                                                                                                    PIR; S24310; S24310.
HSSP; P00323; 2FX2.
                                                                                                                                                                                                                                                                                                            EMBL; X64765; CAA46012.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the thioester dehydratase family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the flavodoxin family. SIMILARITY: Contains 1 flavodoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 SLSIEQI 219
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PRINTS; PR00369; FLAVODOXIN PROSITE; PS00201; FLAVODOXIN PROSITE; PS50902; FLAVODOXII

FLAVODOXIN; 1. FLAVODOXIN_LIKE; 1.

InterPro; IPR008254; Flav nitox synth.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
Pfam; PP00258; flavodoxin; 1.

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                                                                                                                                                                                  Saccharomyces cerevisiae.";
J. Biol. Chem. 257:13081-13087(1982).
I-FUNCTION: This is the heme A-containing chain of cytochrome coxidase, the terminal oxidase in mitochondrial electron transport.
I-CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., I Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirste Kucaba T., Hillier L. W., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Ver Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R. Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cytochrome c oxidase polypeptide VI, mitochondrial precursor (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COX6 YEAST
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DOMAIN 4 143 FLAVODOXIN-LIKE.

SEQUENCE 147 AA; 15186 MW; 5779A72DD1395635
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wright R.M., Rosenzweig B., Poyton R.O.; Occus in Gorganization and expression of the COX6 genetic locus in Saccharomyces cerevisiae: multiple mRNAs with different 3 are transcribed from COX6 and regulated differentially."; Nucleic Acids Res. 17:1103-1120(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-23 FROM N.A. MEDLINE=89160242; PubMed=2537949;
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MEDLINE=85080033; PubMed=6210289;

Wright R.M., Ko C., Cumsky M.G., Poyton R.O.;

"Isolation and sequence of the structural gene for cytochrome oxidase subunit VI from Saccharomyces cerevisiae.";

J. Biol. Chem. 259:15401-15407(1984).
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                                                                              C + 2 H(2)O.
SUBUNIT: Composed of at least 11 subunits.
SUBCELLULAR LOCATION: Mitochondrial inner membrane.
SIMILARITY: Belongs to the cytochrome c oxidase Va family.
                                                                                                                                                                                                                                                                                                                      or I., Tsugita A.; amino acid sequence of cytochrome
                              SWISS-PROT entry is copyright.
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GermOnline; 139368; -.
SGD; S0001093; COX6.
SGO; GO:0005751; C:respiratory chain complex IV (sensu Eukarya); IPI.
GO; GO:0004129; E:cytcothrome-c oxidase activity; IDA.
InterPro; IPR003204; Cyt_c_ox5A.
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15-JUL-1998 (Rel. 36, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Glucose-6-phosphate 1-dehydrogenase (I
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Sarcophagidae; Sarcophaga.
NCBI_TaxID=7385;
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                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bullata (Grey flesh fly) (Neobellieria bullata).
Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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PRINTS; PRO0079; G6PDHDRGNASE PRODOM; PD001129; G6PD; 1. PROSITE; PS00069; G6P_DEHYDROC

9; G6P_DEHYDROGENASE; PARTIAL.
NADP; Glucose metabolism.

InterPro; IPR001282; G6PD

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PF00479; G6PD;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98001474; PubMed=9343309;
Garcia R.L., Sadighi M., Francis S.M., Suttie J.M., Fleming J.
Garcia R.L., Sadighi M., Francis S.M., Suttie J.M., Fleming J.
Garcia R.L., Sadighi M., Francis S.M., Suttie J.M., Fleming J.
Garcia R.L., Sadighi M., Francis S.M., Suttie J.M., Fleming J.
Garcia R.L., Sadighi M., Francis S.M., Suttie J.M., Fleming J.
J. Mol. Endocrinol. 19:173-182(1997).
J. Mol. Endocrinol. 19:173-182(1997).
J. Mol. Endocrinol. 19:173-182(1997).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Neurotrophin-3 precursor (NT-3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is no restrictions of the content is no way use by non-profit institutions as long by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/entities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Antler;
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SEQUENCE
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Pfam; PF00243; NGF; 1.
    Y370 THEMA
Q9WYK4;
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10-OCT-2003 (Rel. 42, I
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Hypothetical UPF0273 pi
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Nelson K.E., Clayton R.A., Gill 5.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Phillips C.A., Richardson D.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heldelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
Salzberg S.L., Smith H.O., Venter J.C., Philips J.C., Philips J.C., Philips J.C., Philips J.C., Philips J.C., Philips J.C., Philips J.C.,
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STRAIN=MSB8 / DSM 3109
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NT3 CHICK
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P25433;
P25433;
O1-MAY-1992 (Rel. 22, Created)
O1-DEC-1992 (Rel. 24, Last sequence update)
O1-DEC-1992 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Neurotrophin-3 precursor (NT-3) (Neurotrophic Neurotrophic 1)
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PIR; H72384; H72384.
TIGR; TM0370; --
HAMAP; MF_01076; --; 1.
HAMAP; MF_01076; --; 1.
ATP-binding; Con
Hypothetical protein; ATP-binding; Con
Hypothetical protein; ATP-binding; Con
Hypothetical protein; ATP-binding; Con
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Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                  MEDLINE=93091238; PubMed=1457809;
Maisonpierre P., Belluscio L., Conover J.C.,
"Gene sequences of chicken BDNF and NT-3.";
DNA Seq. 3:49-54(1992).
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
SEQUENCE OF 194-236 FROM N.A.
MEDLINE=91222573; PubMed=2025430;
Hallboeoek F., Ibanez C.F., Perss
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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30 37 ATP (POTENTIAL).
242 AA; 26813 MW; 396431D4D5E48837 CRC64;
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, Last annotation updat
protein TM0370.
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                         Persson H.;
                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
; Galliformes; Phasiani
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Phasianidae; Phasianinae;
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RESULT 10
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(Nerve growth factory
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Felis silvestris catus (Cat).
Felis silvestris catus (Cat).
Tharyota; Metazoa; Chordata; Cra
                                                                                                                                                                                                                                         NT3 FELCA
Q9TST2;
30-MAY-2000
                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE=20211727; PubMed=10745216;
Lein E.S., Hohn A., Shatz C.J.;
Lein F.S., Forulation of BDNF and NT
                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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CARBOHYD
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Neuron 6:845-858 (1991).
-!- FUNCTION: Seems to promoter and propriocers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                            SEQUENCE
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ProDom; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
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          This SWISS-PROT
                                                        -!- FUNCTION: Seems to promotes the
                                                                       J. Comp. Neurol. 420:1-18(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                development
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the NGF-beta family.
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ROT entry is copyright. It is produced through Swiss Institute of Bioinformatics and the EN
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N-LINKED (GLCNAC. .
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                                                  survival of visceral (By similarity).
                                                                                          expression
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RESULT 11

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Best Local
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P20783;
P20783;
O1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neurotrophin-3 precursor (NT-3) (Neurotrophic
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                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90306351; PubMed=2365067;
Kaisho Y., Yoshimura K., Nakahama
                                                                                                                                                                                                                                                                                                                                       Rosenthal A., Goeddel D.V., Nguyen T., Lewi
Laramee G.R., Nikolics K., Winslow J.W.;
"Primary structure and biological activity
neurotrophic factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00243; NGF; 1.
PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
                                                                                                                                                                                                       growth
                                                                                                                                                                                                                      Jones K.R., Reichardt L.F.; "Molecular cloning of a human
                                                                                                                                                                                                                                                             MEDLINE=91045937; PubMed=2236018;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=90262727; PubMed=2344409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P20783;
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 MEDLINE=91365361; PubMed=1889806;
                 SEQUENCE FROM N.A.
                                                                                           "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                       factor family.";
Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                        4:767-773 (1990).
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                                                      266:187-191 (1990
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NEUROTROPHIN-3.
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5. 37;
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Maisonpierre P.C., ...
Belluscio L., de la
Yancopoulos G.D.;
PROSITE; PSCO<sup>2</sup>48; NGF 1.

NGF 1.

Probom; PD002052; NGF; 1.

SMART; SM00140; NGF; 1.

PROSITE; PS00248; NGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hallboeoek F., Ibanez C.F., Persson H.; "Evolutionary studies of the nerve growth factor family reveal novel member abundantly expressed in Xenopus ovary."; Neuron 6:845-858(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Leukocyte;
MEDLINE=91222573; PubMed=2025430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human and rat brain-derived neurotrophic factor and neurotrophin-3: yene structures, distributions, and chromosomal localizations.";
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Robinson R.C., Radziejewski C., Stuart D.I.,
"Structure of the brain-derived neurotrophic
                                                                                                                                                                                          EMBL; X53655; CAA37703.1; -.
EMBL; M37763; AAA59953.1; -.
EMBL; M61180; AAA63231.1; -.
PIR; A36208; C40304.
PDB; LBND; 04-APR-96.
PDB; 1B8K; 09-FEB-99.
PDB; 11873; 16-JUN-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arinami T., Takekoshi K., Itokawa M., Hamaguchi H., Toru M.; Failure to find associations of the CA repeat polymorphism in the first intron and the Gly-63/Glu-63 polymorphism of the neurotrophin-3 gene with schizophrenia."; psychiatr. Genet. 6:13-15(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 34:4139-4146(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95251647;
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict produced by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys.
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                                                                              GO; GO:0005102; F:receptor binding; GO; GO:0007267; P:cell-cell signalit GO; GO:0007267; P:cell-cell signalit GO; GO:0007267; P:selnal transductic GO; GO:0007165; P:signal transductic InterPro; IPR002072; NGF.

Pfam; PF00243; NGF; 1.
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SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Brain and peripheral tissues.
POLYMORPHISM: Variant Glu-76 (frequently reported thought to be associated with severe forms of schidoes not seem to be the case.
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Monte S.M., Squinto S., Furth
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NGF_2; 1.
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                                                                                                                  transduction; TAS
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MEDLINE-90190865; PubMed-2314473;
MEDLINE-90190865; PubMed-2314473;
Mehohn A. Leibrock J., Bailey K., Barde Y.-A.;
"Identification and characterization of a novel growth factor/brain-derived neurotrophic factor Nature 344:339-341(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (Nerve growth factor 2) (NGF-2).
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01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
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01-FEB-1991
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                           modified and this statement is not remove the statement of the entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           proprioceptive sensory neurons.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Brain and peripheral tissues.
-!- SIMILARITY: Belongs to the NGF-beta family.
  EMBL; X53257; CAA37348.1; PIR; S09155; S09155.
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MGD; MGI:97380; NtI3.

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GO; GO:0045944; P:posi
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30-MAY-2000
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P18280;
                                                                                                                                                                                                          MEDLINE=90208301; PubMed=2321006; Maisompierre P.C., Belluscio L., (Lindsay R.M., Yancopoulos G.D.; "Neurotrophin-3: a neurotrophic fi Science 247:1446-1451(1990).
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=90319130; PubMed=2164684;

Ernfors P., Ibanez C.F., Ebendal T., Olson L., Persson H.;

"Molecular cloning and neurotrophic activities of a protein

structural similarities to nerve growth factor: development

topographical expression in the brain.";

proc. Natl. Acad. Sci. U.S.A. 87:5454-5458(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last Sequence update)
30-MAY-2000 (Rel. 39, Last amotation update)
Neurotrophin-3 precursor (NT-3) (Neurotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00243; NGF; 1.
PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
                                                                               MEDLINE=91365361; PubMed=1889806; Maisonpierre P.C., le Beau M.M., l Belluscio L. de la Monte S.M., SYancopoulos G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                             "Human
                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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GO:0005515; F:protein binding; IPI.
GO:0007420; P:brain development; IMP.
GO:0007421; P:epidermal differentiation; IMP.
GO:0007403; P:glial cell fate determination; IMP.
GO:0007403; P:gripheral nervous system development; IMP.
GO:0007422; P:peripheral nervous system development; IMP.
GO:0007423; P:positive regulation of transcription from
                     structures, distribu
mics 10:558-568(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ve growth factor OR NTF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 KNKLSKQ 458
                                       and rat brain-derived neurotrophic factor and neurotrophin-3:tructures, distributions, and chromosomal localizations.";
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Rodentia;
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N-TINKED ALBARE6042 CI
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Pred. No.
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RESULT 14
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EMBL; M33968; AAA41727.1; -.
EMBL; M63179; AAA63497.1; -.
PIR; A35781; A35781.
HSSP; P20783; 1B8K.
InterPro; IPR002072; NGF.
Pfam; PF00243; NGF; 1.
                                                                                                                                                                     O35740; O35741; O35742; O35743; O55198;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cbp/p300-interacting transactivator 2 (MSG-related
                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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STRAIN=C57BL/6 X DBA;

MEDLINE=98202510; PubMed=9533950;

Dunwoodie S.L., Rodriguez T.A., Beddington R.S.P.;

"Msg1 and Mrg1, founding members of a gene family,

patterns of gene expression during mouse embryogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Evolutionary studies of the nerve growth factor family reveal novel member abundantly expressed in Xenopus ovary."; Neuron 6:484-858(1991).
-i- FUNCTION: Seems to promotes the survival of visceral and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00268; NGF. ProDom; PD002052; NGF; 1. SMART; SM00140; NGF; 1.
                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00248; NGF_1; PROSITE; PS50270; NGF_2;
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Hallboeoek F., Ibanez C.F., Persson H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 195-237 FROM N.A. STRAIN-Sprague-Dawley; TISSUE-Liver;
                                                                  SEQUENCE FROM N.A.
                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proprioceptive sensory neurons.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Brain and p
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5. 37;
  embryogenesis.";
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EMBL; Y15163; CAA75433.1; -.
EMBL; Y15163; CAA75434.1; -.
EMBL; Y15163; CAA75435.1; -.
EMBL; U86445; AAC39945.1; -.
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-!- SUBUNIT: Binds to the p300/CBP CH1 region (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
MEDLINE=98094278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CITED2 OR MRG1
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GO:0007417; P:central nervous
rPro; IPR007576; CITED.
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                                                                                                                                                                                                                                       378
                                                                                                                                                                                                        233
    sapiens (Human).
                                                                                                                                                                                                                                                                   Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72:27-40(1998).
                                                                                                                                                                                                            EMGLDRI 239
                                                                                                                                                                                                                                       EMGLDRI 384
                                                                                                                                                                                                                                                                                                                                  269
                                                                                                                                                                                                                                                                                                                                                                                                                         21
162
218
138
                                                                                                                                                                                                                                                                                                                                                                                            159
                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITED;
                                                                                                                                                                                                                                                                                                                                  ß,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9434189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                                                                           197
257
158
                                                                                                                                                                                                                                                                                                                                                                 213
                                                                                                                                                                                                                                                                                                                                                                                               213
                                                                                                                                                                                                                                                                                                                                    28382 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence=VSP_001091;
                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                       Score 7;
                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                               Missing (i
/FTId=VSP_
                                                                                                                                                                                                                                                                                                                                                                                Missing (i
/FTId=VSP
                                                                                                                                                                                                                                                                                                                                  Missing (In isoform 4).
/FTId=VSP_001092.
AFACDDD5D7902A48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ASP/GLU-RICH
                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system
                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (in
                                                                                                                                                                                                                                                                                                                                                                                                  (In isoform 3).
                                                                                                                                                                                                                                                                                          DB 1;
o. 39;
                                                                                                                                                                                                                                                                                                                                                                                   001091
                                                                                                                                                                                                                                                                                                                                                                                                                   001090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development; IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                 isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                 (ACIDIC).
isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternative splicing.
                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                        Length 269;
                                                                                                                                                                                                                                                                               Indels
                                                                ۲
                                                                                                                                                                                                                                                                               0;
                                                                (MRG1
                                                                                                                                                                                                                                                                                 Gaps
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RX MEDLINE=22388257; PubMed=12477/9432;
RA Strausberg R.L., Feingold E.A., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.D., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.D., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.D., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley N.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley N.C., Shevchenko V., Bouffard G.G.,
RA Rahiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Rahiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Rahiting M., Madan A., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.,
RA Rodriguez C.D., Schein J.E., Jones S.J.M., Marra M.A.,
RA Rodriguez C.D., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and mouse cDNA sequences."
RT human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97057236; PubMed=8901575; Shioda T., Fenner M.H., Isselbacher K.J.; Shioda T., Fenner M.H., Isselbacher K.J.; a novel melanocyte-specific gene, encodes a and is associated with pigmentation."; proc. Natl. Acad. Sci. U.S.A. 93:12298-12303(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leung M.K., Jones T., Michels C.L., Livingston D.M., Bhattacharya S., "Molecular cloning and chromosomal localization of the human CITED2 gene encoding p35srj/Mrgl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional role of p35srj,
transactivation by HIF-1.";
Genes Dev. 13:64-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDJURNCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (ISOFORM 1).
Bhattacharya S., Michels C.M., Leung M.K., Arany Z.P., Kung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jenomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Pancreas;
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
EMBL; U65093; AAC51114.1; ---
EMBL; AF129290; AAF01263.1; ---
EMBL; AF129290; AAF01264.1; ---
                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- INDUCTION: By hypoxia and deferoxamine
-!- SIMILARITY: Belongs to the CITED family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Binds to the p300/CBP CH1 region SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q99967-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q99967-2; Sequence=VSP_001089; DUCTION: By hypoxia and deferoxamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61:307-313 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rya S., Michels (n.D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a novel p300/CBP binding protein, during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2).
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DR EMBL; AF109161; AAD10055.1; -.

DR EMBL; BC004377; AAH04377.1; -.

DR Genew; HGNC:1987; CITED2.

DR MIM; 602937; -.

DR GO; G0:0005634; C:nucleus; NAS.

DR GO; G0:0005515; F:protein binding; NAS.

DR GO; G0:0005700; F:transcription factor activity; TAS.

DR GO; G0:000570; F:regulation of transcription from Pol II pro. ..; TAS.

DR GO; G0:0005776; CITED.

DR InterPro; IPR007576; CITED.

DR Fram; PF04447; CITED.; 1.

KW Transcription regulation; Nuclear protein; Alternative splicing.

FT DOMAIN 162 199 GLY-RICH.

FT DOMAIN 162 199 GLY-RICH. (ACIDIC).

FT DOMAIN 219 258 ASP/GLU-RICH (ACIDIC).

FT DOMAIN 219 258 Missing (in isoform 2).

FT DOMAIN 219 258 Missing (in isoform 2).

FT DOMAIN 219 258 Missing (in isoform 2).

FT SEQUENCE 270 AA; 28497 MW; 45DDE3A9E2B4C472 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 270;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 6, 2004, 19:42:29

Job time: 20 secs
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Copyright

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Word size :
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                                                                                                                                                                                                              Score
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seq length: 2000000000
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Match
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                    sp_plant:*
sp_vrodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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   16
16
16
16
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                                     Q7Z144
Q8FQ52
Q8FQ55
Q9G635
Q7WEP5
Q7W3C6
Q7VU31
Q9FNU1
Q8ZZM7
Q9XS63
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                                                                                                                                                                          Q9LDX1
Q7XYE6
                                                                                                                                                             Q7XY17
                                                                                                                                                                                                                                                  SUMMARIES
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Q9ldx1 arabidopsis
Q7xye6 triticum ae
Q7xy17 triticum ae
Q7x144 caenorhabdi
Q8fq52 corynebacte
Q98bt9 rhizobium 1
Q8g635 bifidobacte
Q7wep5 bordetella
Q7w316 bordetella
Q7w316 bordetella
Q7w131 bordetella
Q9fnul oryza sativ
Q8zzm7 pyrobaculum
Q9xs63 equus cabal
Q81ln5 oryza sativ
Q8r9u3 thermoanaer
Q18097 caenorhabdi
                                                                                                                                                                                                             Description
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Kily von cellering		·	j	}		ť
٥	2	л	163		7	4.5
tπ		10	159	1.1	7	44
ש	o	Ŋ	157	1.1	7	43
Q92tz2 rhizobium		16	152	1.1	7	42
007614 bacillus		16	149	1.1	7	41
φ		11	148	1.1	7	40
σ	Овисие	16	147	1.1	7	39
Q7szf9 fugu rubrip	Q7SZF9	13	147	1.1	7	38
ש		σ	146	1.1	7	37
Q8spt8 macaca mula	Q8SPT8	σ	139	1.1	7	36
067676 aquifex aeo	067676	16	135	1.1	7	35
		11	129	1.1	7	34
Q9mad2 arabidopsis	Q9MAD2	10	126	1.1	7	<u>3</u> 3
Q8n7k2 homo sapien	o	4.	121	1.1	7	32
Q9d2t3 mus muscul	Q9D2T3	11	114	1.1	7	31
Q81342 vibrio chol	o	N	108	1.1	7	30
0		17	101	1.1	7	29
9 xy1	Q87AT9	16	94	1.1	7	28
Q9ns17 homo sapien	Q9NS17	4	93	1.1	7	27
۷ib		16	92	1.1	7	26
2		16	91	1.1	7	25
Q8t9n2 plasmodium	Ø	Ŋ	91	1.1	7	24
. Q9hps2 halobacte		17	69		7	23
Q7vvy4 bordetella	Q7VVY4	16	916		80	22
		16	916	1.3	œ	21
	Q7WGI6	16	916		œ	20
J	Q8S2B7	10	855		8	19
Q8ilz2 plasmodium	Q8I1Z2	ហ	780		8	18
O96148 plasmodium	096148	ហ	616	1.3	8	17

ALIGNMENTS

OSLIDIA OSLIDAI OSCOCT-2000 (TrEMBLIFel. 15, Last sequence update) OT 01-OCT-2000 (TrEMBLIFel. 14, Last sequence update) OT 01-OCT-2000 (TrEMBLIFEL 15, Last sequence update) OT 01-OCT-2000 (TrEMBLIFEL 14, Last sanotation update) OT 01-OCT-2000 (TrEMBLIFEL 15, Last sequence update) OT 01-OCT-2000 (TrEMBLIFEL 15, Last sequence update) OT 01-OCT-2000 (TrEMBLIFEL 15, Last sequence update) OT 01-OCT-2000 (TrEMBLIFEL 15, Last sequence update) ON NCBL TAXID-3002; RASTORY (MODELLE 15, Last sequence Endroyphyta; Core eudicots; rosids; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Spermatophyta; Magnoliophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC Magnoliophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; OC
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EMBL; AF239719; AAF73960.1; -.

EMBL; BT002944; AA022757.1; -.

EMBL; BT004380; AA042374.1; -.

InterPro; IPR005380; XS.

InterPro; IPR005381; zf.
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Li J.R., Wang F., Li Q.Z., Zhang X.S.;
"Gene isolation and expression of a new Zn-finger.";
"Gene isolation and expression of a new Zn-finger.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Q8FQ52;
01-MAR-2003
                                                                                                                               "The entire genomic sequence of Corynebacterium efficiens Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AP005218; BAC18092.1; -.
                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003
01-MAR-2003
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"The sequence of C.
Submitted (JUN-1995)
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Rhabditidae; Peloderinae;
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Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                      CE1282
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STRAIN=Bristol N2;
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01-OCT-2003
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    Conservative
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Score 9; DB 1; Pred. No. 1.9
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EMBL/GenBank/DDBJ
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Pred. No.
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elegans Sequencing Consortium.";
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                      DB 16;
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STRAIN=NCC 2705;

MEDLINE-22294977; PubMed=12381787;

Schell M.A., Karmirantzou M., Snel B., Vil
Pessi G., Zwahlen M.-C., Desiere F., Bork
Pridmore R.D., Arigoni F.;

"The genome sequence of Bifidobacterium lo
to the human gastrointestinal tract.";
                                                                                                                                                                                                      Bifidobacterium longum.
Bifidobacteria; Actinobacteridae; Bifidobacteriales;
Bacteria; Actinobacteria; Actinobacterium.
Rifidobacteriaceae; Bifidobacterium.
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Pfam;
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01-MAR-2003
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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01-JUN-2003 (TrEMBLrel.
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InterPro; IPR006090; Acyl-CoA_dh_C.
InterPro; IPR006091; Acyl-CoA_dh_M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome structure of Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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GO:0003995; F:acyl-CoA dehydrogenase activity;
GO:0015491; F:oxidoreductase activity; IEA.
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PF02770; Acyl-CoA_dh_M; 1.
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ere F., Bork P., Delley
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Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A Cardeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
A Feltwell T., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
A Leather S., Moule S., Sanders M., Saunders D., Seeger K.,
A Rabbinowitsch E., Rutter S., Sanders M., Saunders D.J.;
A Comparative analysis of the genome sequences of Bordetella pertussis,
T "Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
Rembi, BX640451, CAE34951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
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Best Local (
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01-OCT-2003
01-OCT-2003
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EMBL; AE014703; AAN24629.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 212 AA; 25137 MW; EDA495CD83D8B53D CRC64;
                                                                                                                                                                                                                                                                                  Q7W3C6;
Q7W3C6;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=RB50 / ATCC BAA-588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alcaligenaceae;
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7WEP5
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     SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
                                                                                                       Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                 Putative enoy1-CoA
                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                      TaxID=519;
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273 AA;
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Pred. No.
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A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A chtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
A chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
I Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
A Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
A Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
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"Comparative analysis of the genome sequences of Bordetella pertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).

NEMBL, BX640435; CAB39398.1; -.
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10 Nat. Genet. 35:32-40(2003).

11 Nat. Genet. 35:32-40(2003).
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
MEDLINE=22827954; PubMed=12910271;
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Alcaligenaceae, Bordetella.
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RESULT 11 Q9FNU1 ID Q9FNU1

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AC QBZZM
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RX MEDLI
RA Eitz-
RA Mille
RT "Geno
RT "Geno
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RI Inter
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DR SMARI
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RESULT 13
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01-MAR-2001
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01-OCT-2002
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Shiloff B.A., Bennetzen J.L.;
"Comparative sequence analysis of colinear
artificial chromosomes.";
Plant Physiol. 125:1342-1353(2001).
EMBL; AY013245; AAG45493.1; -.
         Q9XS63
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrobaculum aerophilum.
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gramene; Q9FNU1; -. SEQUENCE 296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36I5.S.
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                                                                                                                                                                                                                                                                                                                   261 HRELAEVL 268
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
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8; Conserv
                                                                                                                                                                                                                              HRELAEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acad. Sci. U.S.A. 99:984-989(2002).
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(TYENBLrel. 20, Last sequence update)
(TYENBLrel. 25, Last annotation update)
protein PAE0172.
         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
                                                                                                                                                                                                                                                                                                                                                                                          1.3%; 5c-
100.0%; Pr
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22,
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yta; Liliopsida; Poales; Poaceae;
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02A24E5A2523386F CRC64;
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o. 28;
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5. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 408;
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Best Local
                                                                        SEQUENCE FRUM N....

SERAIN=CV. Nipponbare;

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger P., Jin S.S.,

Buell C.R., Teitrin T., Kim M.M., Bera J.J., Jin S.S.,

Overton II L.L., Teitrin T., Kim M.M., Bera J.J., Jin S.S.,

Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Heiao J., Blunt S.,

Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,

Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,

Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,

White O., Salzberg S.L., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OJI112_G08 genomic sequence.";

"Oryza sativa chromosome 3 BAC OJI112_G08 decomic sequence.";

"Oryza sativa chromosome 3 BAC OJI112_G08 decomic sequence.";
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01-NOV-1999
01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                           Eastman A.P., Smith S.C.,
Cordonnier-Pratt M.-M.;
"Untitled.";
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PROSITE; PS00422; GRANINS_1; 1.
PROSITE; PS00423; GRANINS_2; 1.
SEQUENCE 448 AA; 49861 MW; 1
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InterPro; IPR001990; Granin.
Pfam; PF01271; Granin; 1.
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J. Vet. Med. Sci. 62:953-959(2000).
EMBL; AB025570; BAA76748.l; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equue caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
Submitted (JUN-2003) to the EMBL; AF377947; AAM34395.2;
                                               Buell
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2002) to the
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                                                                 STRAIN=CV.
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                                            R.;
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Hasegawa T., Katayama Y.,
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                                                                 Nipponbare;
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Pred. No.
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Best Local Similarity
Matches 8; Conserv
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C STRAIN=MB4 / JCM 11007;

C STRAIN=MB4 / JCM 11007;

X MEDILINE=21992816; PubMed=11997336;

X MEDILINE=21992816; PubMed=11997336;

X MEDILINE=21992816; PubMed=11997336;

A Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

A Chen Y., Xue Y., Xu Y., Liai X., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

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Hypothetical protein.
SEQUENCE 516 AA; 58268 MW; 0B9B6A77D0273F55 CRC64;
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Q8R9U3;
Q8R9U3;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Dast annotation update)
predicted kinase related to dihydroxyacetone kinase.
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2004, 19:40:52 ; Search time 23 Seconds (without alignments) 1402.880 Million cell updates/sec

Title: US-10-030-829-3
Perfect score: 625

Sequence: 1 MSSRAGPMSKEKNVQGGYRP......EFDBALEQLMYKHGLHNEDD 625

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

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5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22		20	19	18	17	16	15	14	13	12	11	10	9	8	7	0	σ	4	ω	2		Result No.
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1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.3	1.3	1.3	Query
375	361	351	312	300	295	288	283	257	257	257	257	257	257	257	233	175	162	108	102	94	94	94	85	521	418	327	Length
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US-09-107-532A-4312	US-09-489-039A-12349	US-08-688-988-28	US-09-252-991A-31204	9-	US-09-134-000C-5063	US-09-813-918-3	US-09-434-774-6	PCT-US91-06950-4	US-08-451-390-4	US-08-450-842-4	US-08-928-694-4	US-08-910-691-7	US-08-424-826A-4	US-08-451-947-4	US-09-543-681A-4354	US-09-705-621-13	US-09-252-991A-22093	US-09-252-991A-28062	US-09-543-681A-7823	US-09-406-640-31	US-08-658-335B-31	US-08-629-291A-31	US-09-543-681A-4934	US-09-543-681A-5969	US-09-489-039A-8728	US-09-252-991A-30948	ID
Sequence 4312, Ap	e 12349,	Sequence 28, Appl	Sequence 31204, A	æ	e 50	Sequence 3, Appli	e 6,	e 4,	e 4,	e 4,	e 4.	e 7,	e 4,	Sequence 4, Appli	e 4354	Sequence 13, Appl	Ø	e 28062,	e 7823	e 31,	Sequence 31, Appl	e 31, Ap	e 4934,	e 5969,	Sequence 8728, Ap	quence 3	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	6
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	•
1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	
633	630	596	589	578	577	552	530	530	528	519	511	456	454	453	445	395	,
4	4	4	4	w	2	4	4	w	4	4	4	4	4	4	4	4	
US-09-252-991A-26576	US-09-252-991A-19822	US-09-252-991A-26463	US-09-543-681A-6155	US-08-981-215-1	US-08-756-317-13	US-09-252-991A-29652	US-09-356-806-113	US-09-180-852-2	US-09-356-806-8	US-09-489-039A-11591	US-09-252-991A-28608	US-09-543-681A-5516	US-09-813-918-2	US-09-711-164-349	US-09-252-991A-28986	US-09-673-395A-612	(の) (の) (の) (の) (の) (の) (の) (の) (の) (の)
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26576, A	19822, A	26463, A	6155, Ap	 Appli 	13, Appl	29652, A	113, App	2, Appli	8, Appli	11591, A	28608, A	5516, Ap	Appli	349, App	28986, A	612, App	+0000

ALIGNMENTS

SULT 2 -09-489-039A-8728 Sequence 8728, Applic Sequence 8728, Applic Sequence 8728, Applic Sequence 8728, Applic GENERAL INFORMATION: APPLICANT: Gary Bro TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 270 CURRENT FILING DATE: FRICR APPLICATION NO CURRENT FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: NUMBER OF SEQ ID NO 8728 LENGTH: 418 TYPE: PRT ORGANISM: Klebsiell -09-489-039A-8728	Best Local Similarity 100.0%; Pred. No. 17; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 109 GRGRALSR 116	APPLICATION N FILING DATE: R OF SEQ ID NC NO 30948 FH: 327 PR: PBEUdomc NISM: PBEUdomc 2-991A-30948	RESULT 1 US-09-252-991A-30948 ; Sequence 30948, Application US/09252991A ; Sequence 30948, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: 107196.136 ; CURRENT APPLICATION UNMBER: US/09/252,991A ; CURRENT FILING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US/09/257,991A
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RESULT 3
US-09-543-681A-5969
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              US-08-629-291A-31
; Sequence 31, Application US/08629291A
; Patent No. 5959174
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                                                                 RESULT 5
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SEQ ID NO 5969
LENGTH: 521
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
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                                                                                                                                                                                                                                                                                                        SEQ ID NO 4934
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4934, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                    Matches
                                                                                                                                                                                                     Query Match
Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 1.3%; Sometime 1.3%; Sometime 100.0%; les 8; Conservative 0;
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                                                                                                                                                      470 EIMSEKL 476
                                                                                                                   13 EIMSEKL 19
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100.0%; Pred. No. 53;
ive 0; Mismatches
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Pred. No.
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0; Mismatches
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o. 21;
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o. 25;
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SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/08658335B Patent No. 5981703
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    APPLICANT: Hsieh, Ming-Hsiun
TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
NUMBER OF SEQUENCES: 36
                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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Local Similarity 100.0%;
tes 7; Conservative (
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                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                  COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                 STREET:
              APPLICATION NUMBER:
                                                                                                                                                                                                                     ADDRESSEE:
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Coruzzi, Laura A.
Coruzzi, 130,742
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Lam, Hon-Ming
Hsieh, Ming-Hsuin
VENTION: PLANT GLUTAMATE RECEPTORS
EQUENCES: 36
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                                                                                                                                                                                                     E: Pennie & Edmonds
1155 Avenue of the Americas
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Lam, Hon-Ming
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55 Avenue of the Americas
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linear

; Score 7; DB 2 %; Pred. No. 57; 0; Mismatches

DB 2;

Length 94; Indels

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Gaps

0

single

869-9741/8864

5914-050

08-APR-1996

US/08/629,291A

Version #1.30

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US/08/658,335B

FILING DATE:

05-JUN-1996

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US-09-406-640-31
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
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Local Similarity 100.0%; Pred. No. 57
les 7; Conservative 0; Mismatches
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                              NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-082
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
               TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hsieh, Ming-Hsiun
TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/406,640 FILING DATE: 27-Sep-1999 CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                  LENGTH: 94 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                      TELEFAX: (212) 869-9741/8864
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Lam, Hon-Ming
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                   SEQ ID NO: 31:
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Best Local Similarity
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US-09-252-991A-28062
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                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 2709.1002-001
CURRENT PLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28062, Application US/09252991A Patent No. 6551795
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SEQ ID NO 7823
                                                                  Matches
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Patent No. 6605709
                                                                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 102
TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                     LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                543 QNINPSS 549
                              141 ARGGSAQ 147
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42 ARGGSAQ 48
                                                                Similarity 7; Conserv
                                                                  Conservative
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100.0%; Pred. No. 64
ative 0; Mismatches
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100.0%; Pred. No. 57;
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100.0%; Pred. No.
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61;
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RESULT 10 US-09-252-991A-22093 ; Sequence 22093, Application US/09252991A ; Patent No. 6551795

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARGUSINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22093

LENGTH: 162

TYPE: PRI
OPCA****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/705,621
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application U
patent No. 6673355
GENERAL INFORMATION:
APPLICANT: ESTES, MARY
TITLE OF INVENTION: ROT
FILE REFERENCE: P01932U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-705-621-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-705-621-13
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                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
ORGANISM: Proteus mirabilis
US-09-543-681A-4354
                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GARY ERETON

APPLICANT: GARY ERETON

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 4354

LENGTH: 233

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                           Sequence 4354, Apparent No. 660570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 175
TYPE: PRT
ORGANISM: Rotavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0%;
nes 7; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 VVGQQQQ 147
                                                                                                                                                                                                                                                                                                                                                                         102 VVKELRO 108
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7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                         434 VVKELRQ 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVGQQQQ 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09705621
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                                                                                                                                                                                                                                                                                  Application US/09543681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 7; DB 4
100.0%; Pred. No. 90;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROTAVIRUS ENTEROTOXIN NSP4 AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 7; 1
00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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RESULT 13
US-08-451-947-4
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Best Local Similarity
Matches 7; Conserv
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                                                                                                              US-08-451-947-4
밁
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426
FILING DATE: 19-APR-1995
PRIOR APPLICATION UMBER: 08/030
APPLICATION NUMBER: 08/030
                                                       Matches
                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                             FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT AUMBER: 36,700
REGISTRATION NUMBER: 6
                                                                                                                                                                                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GENENTECH, LACON
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
NUMBER OF STATEMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/587707
                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 KLSKONK 168
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                            452 KNKLSKQ 458
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                                                           7;
                                                                           Similarity
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   KNKLSKQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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SYSTEM: PC-DOS/MS-DOS
                                                          1.1%;
ilarity 100.0%;
Conservative (
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                                                                             score 7;
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                                                                  Mismatches
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o. 1.2e+02;
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                                                                                DB 1; Le
o. 1.3e+02;
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                                                                                              Length 257;
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RESULT 14 US-08-424-826A-4

Sequence 4, Application US/08424826A

GENERAL INFORMATION:
APPLICANT: Rosent

Rosenthal, Arnon

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RESULT 15
US-08-910-691-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                         Sequence 7, Application US/08910691 Patent No. 6015552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424,826A

FILING DATE: 19-Apr-1995

CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/240387

FILING DATE: 10-May-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/648482

FILING DATE: 31-JAN-1991

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION UMBER: 07/587707

FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION

ANAME: DATE: 25-SEP-1990
                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                             APPLICANT: WATANABE, Tatsuya
APPLICANT: YOSHITOMI, Sumie
APPLICANT: SASADA, Reiko
TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VE INVENTION: NOVEL NEUROTROPHIC FACTOR NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P1C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
STATE: Massachusetts COUNTRY: US
                                       CITY: Boston
                                                       ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                452 KNKLSKQ 458
                                                                                                                                                                                                                                                                                                                                                                             45 KNKLSKQ 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Le
5. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 257;
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Query Match
Best Local Similarity
Watches 7; Conserve
                                                                                                                                     TOPOLOGY: linear;
MOLECULE TYPE: protein US-08-910-691-7
밁
                                                                                                                                                                                                                                                                           NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 1234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
                                                                                                                                                                                                                           TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/OI
FILING DATE: 19930604
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/910,691 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                           ENGTH:
                    452 KNKLSKQ 458
45 KNKLSKQ 51
                                                                                                                                                                                          amino acid
                                                                                                                                                                                                             257 amino acids
                                                                     Conservative
                                                                 1.1%; Score 7; DB 3; Ler
100.0%; Pred. No. 1.3e+02;
ative 0; Mismatches 0;
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Search completed: April 6, 2004, 19:44:36 Job time : 24 secs

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Title:
Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
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Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	13	12	10	9	8	7	თ	υ	4	w	2	1	Result No.	
7 7	7	7	7 7	7	7	7	8	9	9	9	. 9	9	Score	
11.1	1.1	1:	, <u>, ,</u>	1.1	1.1	1.1	1.3	1.4	1.4	1.4	1.4	1.4	Query	æ
68 8	60	57	u 0.	36	36	18	916	611	382	324	227	223	Query Match Length	
12	12	15	12	10	9	14	12	12	15	12	9	12	DB	
US-10-424-599-228124 US-10-424-599-169910	US-10-424-599-154923	US-10-029-386-316/9	US-10-424-599-250491	US-09-963-693-225	US-09-205-658-225	US-10-225-567A-1514	US-10-282-122A-51413	US-10-425-114-58390	US-10-369-493-12141	US-10-424-599-234018	US-09-738-626-5288	US-10-424-599-234019	ID	
Sequence 228124, Sequence 169910,		Sequence 316/9, A	Sequence 250491,	Sequence 225, App	Sequence 225, App	Sequence 1514, Ap	Sequence 51413, A	Sequence 58390, A	Sequence 12141, A	Sequence 234018,	Sequence 5288, Ap	Sequence 234019,	Description	

RESULT 2 US-09-738-626-5288

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
	257	257	257	253	227	226	219	216	211	196	189	180	173	166	148	141	139	139	138	138	138	136	136	121	104	104	104	94	78	69
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	US-09-788-188-6	US-09-788-188-5	US-08-450-842-4	US-10-029-386-32003	US-10-335-977-5665	US-10-335-977-5666	US-10-282-122A-69066	US-09-861-451A-26	US-10-627-476-128	US-10-425-114-64832	US-10-424-599-283874	US-10-425-114-54097	US-10-424-599-277920	US-10-425-114-72748	-10	US-10-282-122A-51842	US-10-155-886-57	US-10-155-886-55	US-10-155-886-59	US-10-155-886-53	US-10-424-599-177015	US-10-425-114-69428	US-10-425-114-56375	US-10-108-260A-4862	US-10-227-577-650	US-10-091-504-650	US-09-764-869-650	US-10-223-047-31	US-10-424-599-280255 ·	US-10-106-698-5320
-	6	Sequence 5, Appli		32003,	5665,		69	26, A	Sequence 128, App	Sequence 64832, A		Sequence 54097, A	Sequence 277920,	Sequence 72748, A		5184		55,	59,	Sequence 53, Appl	17701	Sequence 69428, A	56375,	4862,	650,	e 650	650,	Sequence 31, Appl	255	Sequence 5320, Ap

ALIGNMENTS

RESULT 1

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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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Publication No. US20020197605A1
                              S
                                                                                                                                                   US-10-424-599-234018
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LENGTH: 227
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
S-09-738-626-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.4%; Score 9; DB Best Local Similarity 100.0%; Pred. No. 3. Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                         APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION UNMEER: US/10/424,599
TILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234018
LENGTH: 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 234018, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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                                                                         Matches
                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                      FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_53342C.1.pep
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                     Local Similarity 100.0%; es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 DSDALDDSD 178
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119
                                    224 ROWHCPACQ 232
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TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKEDA, MASATO
ROWHCPACO 127
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                                                                                                  Score 9; Pred. No.
                                                                                  Mismatches
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o. 3.7;
                                                                                                        DB 12;
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                                                                                    0
                                                                                                                         Length 324;
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RESULT 4

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APPLICANT: Co., Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITTLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
FILLE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 2003-02-28
CURRENT FILING DATE: 2003-02-29
PRIOR APPLICATION NUMBER: US(10/360,039)
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12141
LENGTH: 382
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TOTHER INFORMATION: Clone ID: LIB3079-030-A8_FLI.pep
US-10-425-114-58390
                                                                                                     US-10-282-122A-51413
                                                                                                                            RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 58390
LENGTH: 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                Query Match
                                                          Sequence 51413, Application US/10282122A Publication No. US20040029129A1
                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mesorhizobium loti
APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                       Local Similarity
les 9; Conserv
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                                                                                                                                                                                                                                                                                                   Score 9; DB 12; Length 611; Pred. No. 8.8;
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                                                                                                                                                                                                                                                                                     Mismatches
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Malone, Cheryl

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PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1514
LENGTH: 18
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 51413
LENGTH: 916
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1514, Application US/10225567A Publication No. US20030113798A1
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                                                                                                                                                                                    APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christeine L.
APPLICANT: ROUSh, Christeine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT PEPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
CURRENT FILING NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, H.

FITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LifeSpan Biosciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bordetella pertussis
DRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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o. 1.2e+02
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/ ORGANISM: Caenorhabditis elegans
US-09-205-658-225
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ORGANISM: Caenorhabditis elegans US-09-963-693-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-205-658-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-963-693-225
                                                          PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 225, Application US/09963693 Publication No. US20030181364A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 36
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Patent No.
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Best Local Similarity
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Best Local
                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/09/205,658
PRIOR FILLING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 08/857,076
PRIOR FILING DATE: 1997-05-15
PRIOR APPLICATION NUMBER: 08/888,534
PRIOR FILING DATE: 1997-07-07
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EARLIER FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: 08/888,534
EARLIER FILING DATE: 1997-07-07
EARLIER APPLICATION NUMBER: US98/10080
EARLIER APPLICATION NUMBER: US98/10080
EARLIER FILING DATE: 1998-05-15
NUMBER OF TO NOTE: 1998-05-15
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APPLICANT: Ogg, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/963,693
CURRENT FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruvkun, Gary
APPLICANT: OGG, Scote
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
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7; Conserve
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US-10-424-599-250491
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Best Local Similarity
Matches 7; Conserv
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                                                                                   US-10-029-386-31679
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Best Local &
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CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 31679
LENGTH: 56
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HAnzel, David K.
APPLICANT: HANZEL DAVID R.
TITLE OF INVENTION: HUVAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ. ID NOS: 34288
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TYPE: PRT
ORGANISM: Glycine max
                                                                                                  OTHER INFORMATION: MAP TO AC008974.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.55
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.8
OTHER INFORMATION: SWISSPROT HIT: Q00535, EVALUE 2.80e+00
                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watch 1.1%; Score 7; DB 12; Local Similarity 100.0%; Pred. No. 1e+02; nes 7; Conservative 0; Mismatches
1.1%; Score 7; DB 14; Length 56;
Local Similarity 100.0%; Pred. No. 1e+02;
hes 7; Conservative 0; Mismatches 0; Indels
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0; Mismatches
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          RESULT 14
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NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 3845
LENGTH: 57
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US-10-264-049-3845
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; NAME/KEY: MISC_FEATURE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3845
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Publication No. US20
GENERAL INFORMATION
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                                                                                                                                          ORGANISM: Glycine max FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_110917C.1.pep US-10-424-599-154923
                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 98-21(5322))B
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 154923
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FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR PILING DATE: 2001-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
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Best Local
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Best Local :
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7; Conservative (
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. US20040005579A1
EVEQLVQ 53
                                    EVEQLVQ 27
                                                                       Conservative
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                                                                                              100.0%;
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; Pred. No. 1e+02;
0; Mismatches
                                                                           Score 7; DB 12; L; Pred. No. 1.1e+02; 0; Mismatches 0;
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                                                                                                                     Length 60;
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 169910
LENGTH: 68
TYPE: PRT
ORGANISM: Glycine max
PEATURE:
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US-guence 228124, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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US-10-424-599-169910
Search completed: April 6, 2004, 19:49:22
Job time : 47 secs
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US-10-424-599-169910
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SEQ ID NO 228124
LENGTH: 62
TYPE: PRT
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local S
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)|B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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APPLICANT: Kovalic David K
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FEATURE:
FEATURE:
LOCATION: (1)..(62)
COTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                   561 SSFIEFQ 567
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                                                                                       22 SSFIEFQ 28
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